

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_pzn model

Run on: January 18, 2003, 04:12:19 ; Search time 44.4279 Seconds
(without alignments)
5391.080 Million cell updates/sec

Title: US-09-026-459A-37

Perfect score: 4017
Sequence: 1 MSRLKKYDVAFALFKLER.....TRMQKQKMDSDTSNKEEK 781

Scoring table: BLOSUM62

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Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Processed: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4017	100.0	2994	1 US-08-204-329-2	Sequence 2, Appl1
2	4017	100.0	2994	2 US-08-482-627-4	Sequence 4, Appl1
3	4017	100.0	2994	3 US-08-801-092-3	Sequence 3, Appl1
4	4017	100.0	2994	4 US-09-315-113-3	Sequence 7, Appl1
5	4017	100.0	2995	5 US-08-959-638-7	Sequence 3, Appl1
6	4017	100.0	3332	1 US-08-038-760-1	Sequence 1, Appl1
7	4017	100.0	3332	1 US-08-038-760-2	Sequence 2, Appl1
8	4017	100.0	3332	2 US-08-470-091-1	Sequence 1, Appl1
9	4017	100.0	3332	2 US-08-470-091-2	Sequence 1, Appl1
10	4014	99.9	2994	5 PCT-US94-10357-1	Sequence 1, Appl1
11	4007	99.8	2995	4 US-08-328-673A-7	Sequence 7, Appl1
12	768	19.1	2808	1 US-07-708-962-1	Sequence 1, Appl1

13	763	19.0	2808	2 US-08-152-721B-1	Sequence 1, Appl1
14	729.5	18.2	4853	1 US-08-832-863-1	Sequence 1, Appl1
15	729.5	18.2	4853	2 US-08-832-877-1	Sequence 1, Appl1
16	727.5	18.1	3249	1 US-08-106-493A-1	Sequence 1, Appl1
17	727.5	18.1	3249	4 US-08-429-264-1	Sequence 1, Appl1
18	516.5	12.9	3747	4 US-09-213-293D-2	Sequence 2, Appl1
19	144	3.6	6773	4 US-09-166-350-27	Sequence 27, Appl1
20	143.5	3.6	3763	1 US-07-792-865D-1	Sequence 1, Appl1
21	143	3.6	3593	4 US-09-404-627-3	Sequence 3, Appl1
22	143	3.6	4205	4 US-09-404-627-1	Sequence 1, Appl1
23	140	3.5	8789	4 US-08-328-254-5	Sequence 5, Appl1
24	138	3.4	3883	1 US-08-468-036-33	Sequence 33, Appl1
25	138	3.4	3883	2 US-08-376-843-33	Sequence 33, Appl1
26	138	3.4	3884	4 US-09-541-782-3	Sequence 3, Appl1
27	138	3.4	3884	4 US-09-723-820-3	Sequence 3, Appl1
28	138	3.4	4868	1 US-08-139-937-12	Sequence 12, Appl1
29	138	3.4	4868	5 PCT-US93-11310-12	Sequence 12, Appl1
30	137	3.4	10136	1 US-08-353-700-2	Sequence 2, Appl1
31	137	3.4	10136	5 PCT-US95-16216-2	Sequence 2, Appl1
32	131	3.3	2415	4 US-09-134-001C-2381	Sequence 2381, Ap
33	130	3.2	5893	1 US-08-592-126-54	Sequence 54, Appl1
34	130	3.2	5893	2 US-08-687-080-44	Sequence 44, Appl1
35	127.5	3.2	5181	1 US-08-257-073-10	Sequence 10, Appl1
36	126	3.1	10254	4 US-08-961-527-29	Sequence 29, Appl1
37	121	3.0	5361	4 US-08-973-462-1	Sequence 1, Appl1
38	121	3.0	6152	4 US-08-973-462-2	Sequence 2, Appl1
39	119	3.0	30549	4 US-09-134-001C-322	Sequence 322, App
40	118.5	2.9	3492	4 US-08-923-992A-9	Sequence 9, Appl1
41	117.5	2.9	7493	1 US-08-212-133A-7	Sequence 7, Appl1
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43	117.5	2.9	7493	2 US-08-670-707A-5	Sequence 5, Appl1
44	117.5	2.9	7493	4 US-09-037-601-5	Sequence 5, Appl1
45	117.5	2.9	7493	4 US-09-315-179-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
; GENERAL INFORMATION:
; APPLICANT: SHEPARD, H. M.
; APPLICANT: MEN, SHU F.
; TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
; TITLE OF INVENTION: MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,329
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05866
; FILING DATE: 14-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RENE A. FITTS
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 16930-00040005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cDNA)
US-08-204-329-2

Alignment Scores:

Pred. No.:	0	Length:	2994
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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QY 21 ThrCysGluLeuLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluLeuSer 40
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640 ACATGTGAACCTTATATATTGACACAAACCCAGAGTTCGATATCTACTGAAATTAATTCT 699
QY 41 AlaLeuValLeuLysValSerThrIleThrPheLeuLeuAlaLysGluValLeuGln 60
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700 GCATTGTGCTTAAAGTTTCTTGAGTCACATTTTATACCTTAAAGGGAGATATACAA 759
QY 61 MetGluAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
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760 ATGGAAGATGATCGTGGTATTTTCATTCAGTTAATGCTATGCTCTGACTATTTTAT 819
QY 81 LysLeuSerProPheMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
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820 AACCTTCACCTCCCATGTTCTCTAAGAAACCATATTAACACAGCTGTATACCATTAAT 879
QY 101 GlySerProArgTyrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
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880 GGTTCACCTCGAACCCAGCGAGTCACAAACAGAGTCCAGCGATACCAAAACACACTA 939
QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluIleGluCysAsnIleAspGlu 140
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940 GAAATATGATACAGATATTATTGAAGTCTCTGTAAACAGATGATGTAATATAGATGAG 999
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluLysValThr 160
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1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTATGAAATCTCTGTGACTGTAA 1059
QY 161 SerAsnGluLeuProGluValGluAsnLeuSerLysArgTyrGlnGluIleTyrLeuLys 180
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1060 TCTTAATGAGACTTCAGAGAGTTGAAATCTTCTTAACAGATACGAAAGAAATTAATCTTAA 1119
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnGly 260
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QY 301 LeuGluValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGlnGluArg 320
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Db 1600 GCCTGCGCTCTTGAGTGTATGCGCCACATATGACAGAAAGTACATCTCAGAAATCTGAT 1659
QY 361 SerGlyThrAspLeuSerPheProThrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
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Db 1660 TCTGGAACAGATTTGCTTCCATGATGATCTGAAATGCTTAATTTAAAGCTTTGAT 1719
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QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnHisThrAlaIleAspMetTyrLeu 460
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QY 521 ArgLeuLeuSerGlnHisProGluLeuGlnHisIleIleThrPheLeuPheGlnHisThr 540
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Db 2140 CGCCTTCTGTGACGCCACCAATTTAGACATATCATCTGAGACCCTTTTCCAGCACACC 2199
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Db 2260 ATGTATGCAATATGCAAGTGAAGATATAGACCTTAAATTCAAATCATGTAACAGCA 2319
QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuLysGluGlu 600
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OY 661 ProLeuLysSerProTyLysIleSerGlyLeuProThrProThrLysMetThrPro 680
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OY 681 ArgSerArgIleLeuValSerIleGlyIleUserPheGlyThrSerGlyLysPheGlyLys 700
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OY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGlyIleSerAsn 720
Db 2680 ATAAATCAAGATGGTATGTTCACAGCCAGCCGGTGCTCTCAAAAAGAGTGTGAAGGAAGCAAC 2735
OY 721 ProProLysProLeuLysLysLeuArgPheAspIleGlyIleSerAspGluAlaAspGly 740
Db 2740 CCTCTAAACCATGAAAAAACAATCAAGCTTTGATATTTGAAGGATCAGATGAAGAGATGGA 2795
OY 741 SerLysHisLeuProGlyIleUserLysPheGlnGlnLysLeuAlaGlnMetThrSerThr 760
Db 2800 AGTAAACATCTCCACGAGAGATCCAAATTTCCACACAAACATGCGAAGAAATGACTTCTACT 2855
OY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlyGlu 780
Db 2860 CGAACACGAATGCAAAACCAACAAATGAATGATAGCATGATACCTCAAAACAAGAAAGAG 2915
OY 781 Lys 781
Db 2920 AAA 2922

RESULT 2
US-08-482-627-4
Sequence 4, Application US/08482627
Patent No. 5998134
GENERAL INFORMATION:
APPLICANT: Lee, Wen-Hwa
APPLICANT: Lee, Eva Y-H-P
TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
City: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,627
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,947
FILING DATE: 28-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1707
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
type: nucleic acid

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QY	301	LeuGlyValAlaGlyLeuTrpTrpArgValMetGlySerMetLeuLysSerGluGluArg	320
Db	1480	CTTGGAGTCCGGCTGTATTATACCAGGTAATGGAATCCATGCTTAATATGAAAGAAAGCA	1539
QY	321	LeuSerLLeuGlnAspPheSerLysLeuLeuAsnAspAsnLLeuPheIstMetSerLeuLeu	340
Db	1540	TGTATCCATTCAGAAATTTTATAGCAAACTTCGATATGCAACAATTTTTCATATGTCCTTAATG	1599
QY	341	AlaCysAlaLeuGlnAlaValAlaMetAlaAlaTrpTrpSerArgSerTrpSerGlnAsnLeuAsp	360
Db	1600	GGCTGGCCCTTGGAGTGTGAATGGCCACATATACGACAATATCATCTCGAATCTTGAT	1659
QY	361	SerGlyTrpAspLeuSerPheProTrpLLeuLeuAsnValLeuAsnLeuLysAlaPheAsp	380
Db	1660	TCGGAACAGATTTGTCTCTCCATGGATTCGAATGTGCTTAATTTTAAAGCCCTTGAT	1719
QY	381	PheTrpLysValLLeuGlySerPheLLeuLysAlaGluGlyAsnLeuTrpArgGluMetLle	400
Db	1720	TTTTTAAAGATGATGAAAGTTTATATCCAAAGCAGAAAGCAACTTGACAAAGAAATGATA	1779
QY	401	LysHsLLeuGlnAlaCysArgLinhAlaArgLLeuMetGlySerLeuAlaAlaPheLeuSerAspSer	420
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QY	421	ProLeuPheAspLeuLLeuGlnSerLysAspArgGluGlyProTrpAspHisLeuGlu	440
Db	1840	CCTTTATTTTGGATCTTATTTAAACATCAAAAGACCCAGAAAGGACCACTGTATGCCCTTGAA	1899
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QY	461	SerProValArgSerProLysLysGlySerTrpTrpArgValAsnSerTrpAlaAsn	480
Db	1960	TCCTCTGTAAAGTCTCCAAAGAAAAAGTTCACTACGGCTGTAAATTTCTACGCAAT	2019
QY	481	AlaGluTrpGlnAlaTrpSerAlaPheGlnTrpGlnLysProLeuLysSerThrSerLeu	500
Db	2020	GCAGAAACCAAGCAACCTCGCCCTCCAGACCAGAAAGCCATTTGAATATACCTCTCTT	2079
QY	501	SerLeuPheTrpLysLysValLysTrpArgLeuAlaTrpLeuAspLeuAsnTrpLeuCysGlu	520
Db	2080	TCACCTGTTTATAAAAAGTGTATCGGTACGACCTATCTCCGGTAAATATACCTTTGTGA	2139
QY	521	ArgLeuLeuSerGlnHisArgGluLeuGlnGlnHisLLeuIleTrpTrpLeuPheGlnHisTrp	540
Db	2140	CGCCTTCCTGTGAGAACCCGAAATTTAGAACATATCATCTGTGACCCTTTTCCAGCACACC	2199
QY	541	LeuGlnAsnGluTrpGluLeuMetArgAspArgHisLeuAspGlnLLeuMetCysSer	560
Db	2200	CTCCCAAAAGATATGAATCAATCAAGACAGACAGCATTTGGACCAAAATTAATGATGTGTCC	2259
QY	561	MetTrpGlyLLeuCysLysValLysAsnLLeaAspLysLysPheLysLLeuLValThraAla	580
Db	2260	ATGTATGGCATGTGCAAAAGTGAAGATATATGACCTTTAAATTCAAATCATTTGAACAGA	2319
QY	581	TrpLysAspLeuProHisAlaValGlnGluTrpPheLysArgValLeuLleLysGluGlu	600
Db	2320	TTCAAAGATCTTCCCAATGCGTCCAGGAGACATTCAAACCTGTTTGTATCAAAAGAACAG	2379
QY	601	GluTrpAspSerLLeuLValPheTrpAsnSerValPheMetGlnArgLeuLysTrpAsn	620
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QY	641	SerProTrpLysPheProSerSerProLeuArgLLeuProGlyLysAsnLLeuTrpLLeuSer	660

Db	2500	AGCCCTTACAGTTTCCAGTTCACCCCTTAGCGATTCCTGGAGGAAACATCTATTTC	2559
Qy	661	ProLeuLysSerProTyrTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro	680
Db	2560	CCCCCTAAGACGCATATATAAATTTGAGAGGTCGCGACACACACAAAAAGATCCCA	2619
Qy	681	ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlyLysPheGlnLys	700
Db	2620	AGATCAAGATCTTAGTATCAATTTGGTGAATCATTTGGGAGCTTGTGCAAGTTCCAGAAA	2679
Qy	701	IleAsnGlnMetValCysAsnSerAspArgValIleuLysAlaGlySerAlaGlnGlySerAsn	720
Db	2680	ATTAATCAAGATGGTATGTATGACAGCGACCGTGGCTCAAAAAAATGTGTGAAGGAGCAAC	2739
Qy	721	ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly	740
Db	2740	CCCTCTTAACCACTGTAATAAAACTATACGCTTTGATATTGAAGGATCAATGAAAGAGATGGA	2799
Qy	741	SerLysHisLeuProGluGlyGluSerLysPheGlnGlnLysLeuAlaGluIleThrSerThr	760
Db	2800	AGTAACACATCTCCACGGAGAGTCCCAAAATTCAGCGAAGAACTGGGACGAAATGAATCTCTCT	2859
Qy	761	ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetLaspThrSerAsnLysGluGlu	780
Db	2860	CGAACCGCAATCCAAAGACGAAAAATGATGTATGATCATGATCATCTCAAAACAAGGAAG	2919
Qy	781	Lys Thr	
Db	2920	AAA	2922

RESULT 3
 US-08-801-092-3
 Sequence 3, Application US/08801092
 Patent No. 6074850
 GENERAL INFORMATION:
 APPLICANT: Antelman, Douglas
 APPLICANT: Gregory, Richard J.
 APPLICANT: Wils, Kenneth N.
 TITLE OF INVENTION: Tissue Specific Expression of
 TITLE OF INVENTION: Retinoblastoma Protein
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSEND AND CREW LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,092
 FILING DATE: 14-FEB-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/751,517
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Flits, Renee A.
 REGISTRATION NUMBER: 35,136
 REFERENCE/DOCKET NUMBER: 016930-001020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-576-0200
 TELEFAX: 703-576-0300
 INFORMATION FOR SEQ. ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2994 base pairs
 type: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-801-092-3

Alignment Scores:

Pred. No.:	0	Length:	2994
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-026-459a-37 (1-781) x US-08-801-092-3 (1-2994)

QY 1 MetSerArgLeuLeuLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
DB 580 ATGTCAAGACTGTGAAGAATGATGATGTTGACCTCTCGCAAAATGGAAAG 639
QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
DB 640 ACATGGAACCTTATATATTGACACACACAGTCGATGCTAATCTGAATAATTAATCT 699
QY 41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
DB 700 GCATGTGCTAAAGTTCTTGATCACAATTTTATTAGCTAAAGGCGAAGTATTACA 759
QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
DB 760 ATGGAAAGATGATCTGTGATTTTCATTTTCAGTTAATCTGTGCTTACATTTTAT 819
QY 81 LysLeuSerProPromeLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
DB 820 AAACCTCCACCTCCACCTGATGCTCAAGAACCATATATAACGCTGTATACCATTAAT 879
QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
DB 880 GGTTCCACCTCGAACACCGGCGAGGTGAGAACAGAGAGTCACGAGTAGCAAAACACTA 939
QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
DB 940 GAAATGATCAACGAATTTATGAAGTCTCTGTAAAGAACATGATATATAGATGAG 999
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
DB 1000 GTCAAAAATGTTTATTTCAAAAATTTTATACCTTTATGATATCTCTGCACTTTGAA 1059
QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
DB 1060 TCTAATGACTTCACAGGTTGAAATCTTCTTAACGATACGAGAAATTTATCTTAA 1119
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
DB 1120 AATTAAGATCTAGATGCAAAATTTATTTTGATCATGATAAACCTCTCGACTGATTC 1179
QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
DB 1180 ATGAGACGTTTGAACACAGACAGAACCCGAAAGAAAGTAACTGTATGAGAGGTGAAT 1239
QY 221 ValIleProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
DB 1240 GTAAATTCCTCCACACTCCAGTTAGAGCTGTATGAAACCTATCCAACTAATTAATGATG 1299
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
DB 1300 ATTTTAATTCAGCAATGATCAACCTTCAGAAATCTGATTCCTATTTTAACAATGCG 1359
QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
DB 1360 ACACTGATCCAAAGAAAGATGACTGAAAAAGATGAAGATATATGATCACTTTTAA 1419
QY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300

DB 1420 GAGAAATTTGCTAAAGCTGTGGACAGGCTTGTCGAAATTTGATCACAGCATACAA 1479
QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
DB 1480 CTTCGAGTTCCTGTTGATTAACCGAGTAATGGAATTCATGCTTAATCAGAAGAACGA 1539
QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
DB 1540 TTATCCATTCAAAATTTTACCAAACTTCGTGAATGACAACTTTTTCATATGCTTTATTTG 1599
QY 341 AlaCysAlaLeuGluValAlaValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
DB 1600 GCGTGGCTCTTGAGAGTTGTATATGCCACATATAGCGAAGTACATCTCGAATCTTGAT 1659
QY 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
DB 1660 TCTGGACAGATTTTGCTTCTCCATGATGCTGAATGCTTAATTTAAAGCCTTTGAT 1719
QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluLysAsnLeuThrArgGluMetIle 400
DB 1720 TTTTACAAAGTATCGAAGGTTTATCAAAAGCAAGGCAACCTTGACAGAGAAATGATA 1779
QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
DB 1780 AAACATTTAGAACATGTCGAACATCGAATCATGGAATCCCTTGATGGCTCTGATTTCA 1839
QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
DB 1840 CCTTATATTTGATCTTATTAACAAATCAAGACGAGAGAACCACTGATCACCTTGAA 1899
QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnHisThrAlaAlaAspMetTyrLeu 460
DB 1900 TCTGTTTCTCTTAACTTCTCTCCAGATATTCACACTGACGAGATATGATCTT 1959
QY 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
DB 1960 TCTCTGTAAAGATCTCCAAAGAAAAGTTCACTACGCGTGAATTTACTAGCAAT 2019
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
DB 2020 CGAGAGACCAAGCAACTCACCTCCAGACCCGAGAGCAATGAAATCTCACTCTCT 2079
QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGluGlu 520
DB 2080 TCACGTGTTTATTAATAAAGTGTATCGCTAGCTATCTCCGGCTTAATACACTTTGTCA 2139
QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTyrThrLeuPheGlnHisThr 540
DB 2140 CGCCTTCTGTGAGACACCAAGATTAGAACATATCATCTGGACCTTTTCAGACACAC 2199
QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
DB 2200 CTTCGAAATGATATGAACTCATGTAGAGACAGGCACTTTGGACAAATATATGATGTTGC 2259
QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
DB 2260 ATGTATGCAATTCGCAAACTGAAGATATAGACCTTAATTTCAAAATATATGTAACACA 2319
QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
DB 2320 TACAAGGATCTTCATCATCTGTCAGAGACATTCAAACGTTTGATCAAAAGAGAG 2379
QY 601 GluTyrAspSerIleIleValaPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
DB 2380 GAGTATGATTCATATATATATATATTAATCTGGCTTCATGCAAGAGCTGAAAACAAT 2439
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
DB 2440 ATTTTCAGATATGCTTCCACAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTGA 2499
QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
DB 2500 AGCCCTTACAAAGTTCTCTAGTTACACCTTACGAGATTCCTGAGGAGAACATATATTTCA 2559

SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
US-09-315-113-3			
Alignment Scores:			
Pred. No.:	0	Length:	2994
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0
US-09-026-459A-37 (1-781) x US-09-315-113-3 (1-2994)			
QY	1	MetSerArgLeuLeuValysTyrAspValLeuPheAlaLeuPheSerIlysLeuGluArg	20
DB	580	ATGTCAAGACGTTGTAAGAAAGTATGATGTATGTTTCACACTTCCACCAATTTGGAAAGG	6399
QY	21	ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer	40
DB	640	ACATGTGAACCTAATATATTTTACACCAACCAGCGTTCGATATCTACTGAAATTAATTC	6999
QY	41	AlaLeuValIleLeuLysValSerTrpIleThrPheLeuLeuAlaIysGlyIleValLeuGln	60
DB	700	GCATTGGCTCAAAAAGTTCTTCGATACATTTTATTACTTAAAGGGGAAGTATACAA	7599
QY	61	MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle	80
DB	760	ATGGAAGATGATCTGGTGATTTCTTCAGTTATGCTATGTGTCCTGACTATTTATTT	819
QY	81	LysLeuSerProPheMetLeuLeuLysGluProTyrIysThrAlaValIleProIleAsn	100
DB	820	AAACTCTACCTCCCAAGTGGCTCAAGAAACCATATTAACACCTGTTATACCATTAAT	8799
QY	101	GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaIysGlnLeu	120
DB	880	GGTTCACCTCGAACAACCCAGCGAGCTCACAACAAGAGTACAGGATAGCAAAACACTA	939
QY	121	GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu	140
DB	940	GAAATATATCAAAATATTTGAAGTTCTCTGTAAGAACATCAATGATATATAGATGAG	999
QY	141	ValLysAsnValTyrPheLysAsnPheIleProPheMetLysSerIleuGlyLeuValThr	160
DB	1000	GTGAAAATGTTTATTTTCAAAAATTTTATACCTTTATGAAATCTCTGGACTGTGMAA	1059
QY	161	SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluIleTyrLeuLys	180
DB	1060	TCTAATGACTTCACAGAGGTGAAGATCTTCTTAACAGATACCAAAATTTATCTTAA	1119
QY	181	AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer	200
DB	1120	AATTAATATGTATGATGCAACATTTATTTTGGATCAATGATTAACCTCTCAGACTGATCT	1179
QY	201	IleAspSerPheGluThrArgIleArgThrProArgLysSerAsnLeuAspGluGluValAsn	220
DB	1180	ATGAGACGTTTGAACACACGAGAACAACACGAAAAAGTAACTTGATATAGAGGGTAA	1239
QY	221	ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet	240
DB	1240	GTAATTCCTCCACACACTCCAGTTAGACTGTATGACATATCCAAATTAATGATG	1299
QY	241	IleLeuAsnSerLysSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys	260
DB	1300	ATTTTAAATTCACCAAGATATCAACCTTGAGAAAACTGATTTCTATTTTAAACAACGCG	1359
QY	261	ThrValAsnProLysLysSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys	280
DB	1360	ACAGTGATTCACAAAAGATATCTAGAAAAGAGTAAAGATATGAGATACCTCTTTAA	1419
QY	281	GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys	300
DB	1420	GAGAAATTTTGCTAAACGCTGGGACAGGGTGTGTGCGAATTTGGATTCACAGGATACAA	14799

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Oy 301 LeuGlyValArgLeuTyrTyrArgValMetGlnSerMetLeuYsSerGlnGlnGluArg 320
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Db 1480 CTTGAGCTTGGCTTGTATACGAGATATGGAATCCATGCTTAATCAAGAAAGAGAGA 1539
Oy 321 LeuSerIleGlnAsnPhseSerYsLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
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Db 1540 TTATCCATCAAAATTTTGAACAACTCGAATGCAACAATTTTCATATGCTTATATG 1559
Oy 341 AlacYsAlaLeuGlnValValMetAlaThrTyrSerIleSerGlnSerGlnAsnLeuAsp 360
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Db 1600 GCGTGCCCTCTTGAAGTTGTAATGCGCACATATGCAAGATCACTCAAGATCTTGAT 1659
Oy 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuYsAlaPheAsp 380
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Db 1660 TCTGGAACAGATTTGCTTCCATGGAATGCTGAATGCTGTAATTAAGCCCTTGAT 1719
Oy 381 PheTyrYsValIleGlnSerPheIleYsAlaGlnGlnYsAsnLeuThrArgGlnMetIle 400
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Db 1720 TTTTACAAGTGAATCGAAAGTTTATCAAGACAGAGCAACTTGACAAAGATA 1779
Oy 401 LysHisIleGlnGluArgCysGlnHisArgIleMetGlnSerLeuAlaTrpLeuSerAspSer 420
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Db 1780 AAAACATTTAGACAGATGTGACATGCAATGCAATGCCATGCCATGGCTCTCAAGATTCA 1839
Oy 421 ProLeuPheAspLeuIleYsGlnSerYsAspArgGlnGluProThrAspHisLeuGln 440
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Db 1840 CTTTATTTGATCTTATTAACATCAAGAGCCAGAAAGACCAACTGATCACTTGAA 1899
Oy 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetYrLeu 460
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Db 1900 TCTGCTGTCCTCTTATATCTCTCCAGATATATCACTGACAGCAGATATGATCT 1959
Oy 461 SerProValArgSerProYsYsYsGlnSerThrThrArgValAsnSerThrAlaAsn 480
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Db 1960 TCTCTGTAAGATCTCCAAAGAAAAGGTTCACTACGCTGTAATCTACTGCAAT 2019
Oy 481 AlaGlnThrGlnAlaThrSerAlaPheGlnThrGlnYsProLeuYsSerThrSerLeu 500
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Db 2020 GAGAGACACAGACACCTGAGCTTCCAGACCCAGAAAGCATTGAAATCTACTCTCT 2079
Oy 501 SerLeuPheTyrYsYsValYrArgLeuAlaYrLeuArgLeuAsnThrLeuYsGln 520
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Oy 521 ArgLeuLeuSerGlnHisProGlnLeuGlnHisIleIleTrpThrLeuPheGlnHisThr 540
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Db 2140 GCGCTGTGCTGTGAGCACCCAGAAATTAGAACATATCATCTGGACCTTTCCAGACACC 2199
Oy 541 LeuGlnAsnGlnYrArgIleuMetArgAspArgHisIleAspGlnIleMetMetCysSer 560
    |||
Db 2200 CTGCGAATGAGTATGAACTCATGAGAGACAGGCAATTTGGACCAAAATTAGATGTGTCC 2259
Oy 561 MetYrGlnYleCysYsValYsAsnIleAspLeuYsPheYsIleIleValThrAla 580
    |||
Db 2260 ATGTATGGCATATGCAAGAGAAATATAGACTTAATTAATCAAAATCATTTGACACGA 2319
Oy 581 TyrYsAspLeuProHisAlaValGlnGlnYrPheYsArgValLeuIleYsGlnGln 600
    |||
Db 2320 TACAAGATCTTCTCATGCTGTTCCAGAGACATCAAAAGCTTTTGTATCAAAAGAGAG 2379
Oy 601 GlnYrAspSerIleIleValPheYrAsnSerValPheMetGlnAsnArgLeuYsThrAsn 620
    |||
Db 2380 GAGTATGATTTATATAGATCTTATACCTGAGCTTCAAGCAAGAACGAAACAAAT 2439
Oy 621 IleLeuGlnYrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
    |||
Db 2440 ATTTTGGAGTATGCTCCACAGGCCCCCTACCTGTGTACCAAAATCCCAATTCCTCGA 2499
Oy 641 SerProYrYsPheProSerSerProLeuArgIleProGlnYsAsnIleYrYsIleSer 660
    |||
Db 2500 ACCCTTACAAAGTTTCTAGTCAACCTTACGATTCCTGAGAGGAAACATCTATATTCA 2559
Oy 661 ProLeuYsSerProYrYsIleSerGlnGlnYsLeuProThrProThrYsMetThrPro 680
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Db 2560 CCCCTGAAGGTCATATTAATTTTACAGAGTCTGTGCAACACCAACAAATGACTCTCA 2619
Oy 681 ArgSerArgIleLeuValSerIleGlyIleSerPheGlyThrSerGlnYsPheGlnYs 700
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Db 2620 AGATCAAGAAATCTTATATCAATATGCTGAATCATATTCGGGACTTCTGACAAAGTCCAGAAA 2679
Oy 701 IleAsnGlnMetValCysAsnSerAspArgValLeuYsArgSerAlaGlnYsSerAsn 720
    |||
Db 2680 ATAAATGAGTGTATGTATACAGGACCGCTGTCTCAAAAAGAAAGTCTGAAGAAAGAAC 2739
Oy 721 ProProYsProLeuYsYsYsLeuArgPheAspIleGlnGlnYsSerAspGlnAlaAspGly 740
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Db 2740 CTTCTTAACCACTGAAAAAACTACGCTTGATATGTGAAGATCAATGACAGATGGA 2799
Oy 741 SerYsHisLeuProGlnYsIleSerYsPheGlnGlnYsLeuAlaGlnMetThrSerThr 760
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Db 2800 AGTAAACATCTCCAGAGAGTCCAAATTTCCAGCAGAACTGCAAAATGACTTCTACT 2859
Oy 761 ArgThrArgMetGlnYsGlnYsMetAsnAspSerMetAspThrSerAsnYsGlnGlu 780
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Db 2860 CGAACAGAAATGCAAAAGCAAAATGAATGATGATGATGATGATGATGATGATGATGATGAT 2919
Oy 781 Lys 781
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Db 2920 AAA 2922

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RESULT 5
 US-08-959-638-7
 ; Sequence 7, Application US/08959638
 ; Patent No. 5932210
 ; GENERAL INFORMATION:
 ; APPLICANT: Gregory, Richard J.
 ; APPLICANT: Wills, Ken N.
 ; APPLICANT: Maneval, Daniel C.
 ; TITLE OF INVENTION: Recombinant Adenoviral Vector and
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/959, 638
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/328, 673
 ; FILING DATE: 25-OCT-1994
 ; APPLICATION NUMBER: US 08/233, 777
 ; FILING DATE: 19-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/142, 669
 ; FILING DATE: 25-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-CJ 1192
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2995 base pairs
 ; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 139..2922
; US-08-959-638-7

Alignment Scores:
Pred. No.: 0 Length: 2995
Score: 4017.00 Matches: 781
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-026-459a-37 (1-781) x US-08-959-638-7 (1-2995)

QY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
580 ATGTCAAGACGTGTGACAGAGTAGATGATGTGTGACCTCTCCAGCAAAATTCGAAAGC 639
QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
640 ACATGTGACATTATATATTATTCACACACACAGCAGTTCATATCTAGCAAAATTAATTC 639
QY 41 AlaLeuValLeuLysValSerTyrIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
700 GCATGTGTCTAAAGATTCTTGATCACAATTTTATATAGCTAAAGGGGAAATTTTACA 759
QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
760 ATGCAAGATGATCTGTGATTTCAATTCATCTATATGCTATGCTCTCCGACTATTTTAT 819
QY 81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
820 AAATCTCTACCTCCCATGTCTCAAGAACCATATAAACAGCTGATATACCATTAAT 879
QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
880 GGTTCACCTCGAACACCGACGCGAGTCNAACNAGNAGTCACGGATGCAAAACAACTA 939
QY 121 GluAsnAspThrArgIleIleGlnValLeuCysGluHisGlyCysAsnIleAspGlu 140
940 GAATAATGATACAAAGAAATTAATGAAATCTCTGTGAAAGAACATGAATATATATGATG 999
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
1000 GTGAAAAATGTTATTTCAAAAAATTTTATACCTTTATGAAATTTCTCTGGACCTGTAA 1059
QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
1060 TCTAATGACCTCCAGAGGTGAAATCTTTAAACGATACGAAATTAATTAATCTTAA 1119
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1120 AATAAAGATCTAGATGCAACATTAATTTTGTGATCAGATAAATCTTCCACACGATCT 1179
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1240 GTAAATCTCTCCACACACTCCAGTTAAGCATGTTATGAAACATATCCAAACATTAATAT 1299
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
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QY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
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QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
1480 CTGGAGTTCGCTTGATTAACGAGTAATGCAATCCATGCTTAATATCAGAAAGAACGA 1539
QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
1540 TTATCATCTCAAAATTTTACCAAACTTCTGAATGCAACAACTTTTCATATGCTTATATG 1599
QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
1600 GGTTCGCTCTTGAGGTGTGAATGCGCATATATGAGAAAGTACATCTCAGAAATCTGAT 1659
QY 361 SerGlyThrAspLeuSerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
1660 TCTGCAACAGATTTTGCTTTCCTCCATGAGATTCGAATGTGCTTAATTAAGCCCTTGAT 1719
QY 381 PheTyrLysValIleGlnSerPheIleLysAlaGluGlnValLeuThrArgLysLeuIle 400
1720 TTTTCAAAAGTANTCGAAAGTTTATCAAAAGCAGAGCAACTTGACAAAGAAATGATA 1779
QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaThrLeuSerAspSer 420
1780 AAACATTTAGACAGATGTACATCAATCAATGAAATCCCTTCATGCTCTCAGATTCA 1839
QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluLysProThrAspHisLeuGlu 440
1840 CTTTATTTGATCTTATTAACAAATCAAGACCGCAAGACCAACCACTATACCTTGAA 1899
QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaIleAspMetLysLeu 460
1900 TCTGCTGTCTCTTATCTCTCTCTCCAGAAATATACACTCGACACATATGATATCTT 1959
QY 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAsn 480
1960 TCTCTGTGAAGATCTCCAAAGAAAGAAAGTTTCACATCGCGGTATATCTCTGCAAA 2019
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
2020 GCAGAGACACAGCAACCTCAGCTTCACAGCCAGAAAGCAATTAATTAATCTCTCTCT 2079
QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
2080 TCACGTGTTTATTAAGAAAGTATGCGCTACCTATCTCGGCTTAATACATTTGTGAA 2139
QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheLeuPheGlnHisThr 540
2140 CGCCTTCTGTCTGACACCCAGAAATTAAGACATATCATCTGAGCCCTTTCCAGCACAC 2199
QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
2200 CTGCAAGATGAGATGACTCATGATGACAGACAGCAATTTGACAAATTAATGATGTTCC 2259
QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
2260 ATGATATGCAATGCAAGAGGAAATATAGACCTTAATTAATCAATTTATACACACA 2319
QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGln 600
2320 TCAAGAGATCTCTCATGCTCTGTCAGAGACATTCAAAGSTTTTGATCAAAAGAAAG 2379
QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
2380 GAGTATGATTTCTATATATGATATCTATATACCGGTCTTCATCGAGAGACTGAAACAA 2439
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
2440 ATTTTGCATATGCTTCCACAGGCCCTTACCTGTGCACCAATATCACTTCTCTGA 2499
QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660

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Db 964 GAGAAATTTGCTAAAGCTGTGGACAGGGTTGTGCGAAATGTGATCACAGCATACAAA 1023
 QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuysSerGluGluGluArg 320
 Db 1024 CTTGGAGTTCGGTTTATATACCGAGTAAAGGATCCATGCTTAAATCAGAGAAAGACAA 1083
 QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
 Db 1084 TTATCCATTTCAAAATTTTACCAAACTCTGATGACAACTTTTTCATATGTCCTTATATG 1143
 QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerGlnSerGlnAsnLeuAsp 360
 Db 1144 GCGTCCGCTTTGAGGTTGTATATGCCATATAGCAGAAAGTCAATCTCGAAATCTTGAT 1203
 QY 361 SerGlyThrAspLeuSerPheProTrrIleLeuAsnValLeuAsnLeuysAlaPheAsp 380
 Db 1204 TGTGGACAGATTTGCTTCCATGAGTCTGAAATGCTTATATTTAAAGCCTTTGAT 1263
 QY 381 PheTyrIysValIleGluSerPheIleLysAlaGluGluLysAsnLeuThrArgGluMetIle 400
 Db 1264 TTTTCAAAAGTATCGAAAGTTTATATCAAGCAGAAAGCAACTTGACAGAGAAATGATA 1323
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
 Db 1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTCATGGCTCTCAGATTC 1383
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 Db 1384 CCTTATTTGATCTTATTAACATCAAGACCGAGAAAGCAACACTGATCCCTTGAA 1443
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAspMetTyrLeu 460
 Db 1444 TCTGCTTGCCCTTAACCTCTCTCTCCAGAAATATACACTCCAGAGATATGATCTT 1503
 QY 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
 Db 1504 TCTCCTGTAGATCTCCAAAGAAAAAGTTCACTACGCGTGAAATTTCTACGCAAT 1563
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuysSerThrSerLeu 500
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 Db 1624 TCACGTGTTTAAATAAAGTGTATCGGTATGACCTATCTCCGGCTAAATACACTTGTGA 1683
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheLeuPheGlnHisThr 540
 Db 1684 CCGCTTCTGTGACACCCAGAAATAGAACATATCATCTGAGACCCCTTTCCAGCACAC 1743
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetLysSer 560
 Db 1744 CCGCAAGATAGATGAACTCATGAGACAGCATTTGGACCAAAATTAATGATGTCTTC 1803
 QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuysPheLysIleIleValIleAla 580
 Db 1804 ATGTATGGCATATGCAAAAGTAAAGATATAGACCTTAATTAATTAATCATGTAAACGA 1863
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
 Db 1864 TACAAAGATCTTCCATACGCTTCAGAGACATTCAAAGCTGTTTGAACAAAGAAAG 1923
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 Db 1924 GAGTATGATCTATATATATGATATCTATTAATCTCTTCAATGAGAGACGAAACAAAT 1983
 QY 621 IleLeuGlnIleTyrAlaSerThrArgProThrLeuSerProIleProHisIleProArg 640
 Db 1984 ATTTGCGATATGCTTCCACAGGCCCCCTTACCTGTACACATACCTCATCTCTCGA 2043
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
 Db 2044 ACCCCTTACAGTTTCTAGTTCAACCCCTTACGATTCCTGAGAGAAACATATATTTCA 2103

QY 661 ProLeuysSerProTyrLysIleSerGluGluLeuProThrProThrLysMetThrPro 680
 Db 2104 CCCCTGAAGATGCCATATATTAATTTTCAAGAGTCTGCCAACCAACAAAAATGATCTCA 2163
 QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
 Db 2164 AGATCAAGATCTTATGATCAATTTGTAATTCATTCGAGACTTCTGAGAAAGTTCCAGAAA 2223
 QY 701 IleAsnGluMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGluSerAsn 720
 Db 2224 ATAAATCAGATGGTATGTATACAGCCAGCCGTGCTCAAAAATACTGTCGAAAGAACAC 2283
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
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 QY 761 ArgThrArgMetGluLysGlnLysMetLysAspSerMetAspTrpSerAsnLysGluGlu 780
 Db 2404 CGAACACGATGCAAAAGCAGAAATGATATGATGATGATGATGATGATGATGATGATGATG 2463
 QY 781 Lys 781
 Db 2464 AAA 2466
 RESULT 7
 US-08-038-760-2/c
 Sequence 2, Application US/08038760
 Patent No. 5496731
 GENERAL INFORMATION:
 APPLICANT: Xu, Hong-Ji
 APPLICANT: Hu, Shi-Xue
 TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
 TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/038,760
 FILING DATE: 19930325
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Polissant, Brian M
 REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 7409-025-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8664
 TELEFAX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3232 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: not relevant
 MOLECULE TYPE: DNA
 US-08-038-760-2

Alignment Scores:

Pred. No.: 0 Length: 3232
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservatve: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-026-459a-37 (1-781) x US-08-038-760-2 (1-3232)

QY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGlu 20
 DB 3113 ATGCAAGACTGTTGGAAGAGTATGATGATGTTGGCCTTTGACGAATTTGGAAGG 3034
 QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerLysSerThrGluLeuAsnSer 40
 DB 3053 ACAATGTAACCTTATATATTTGACACCAACCAGAGTTCATATCTACGAAATAAATCT 2994
 QY 41 AlaLeuValLeuLysValSerTrpIleThrPheLeuAlaLysGluValLeuGln 60
 DB 2993 GCATTTGCTTAAAGTTTCTTGATCACAATTTTATAGCTAAAGGGGAAGTATTACA 2934
 QY 61 MetGluAspLeuValIleSerPheGlnLeuMetLysValLeuAspTyrPheIle 80
 DB 2933 ATGGAAGATGATCTGGTATTCATTTCAATTAATGCTATGTGCTTGACTATTTAT 2874
 QY 81 LysLeuSerProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
 DB 2873 AATCTCACCTCCCATGTTGCTGCTCAAGAACATATAAACAGCTGTTATACCCATTA 2814
 QY 101 GlySerProArgThrProArgArgGluGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
 DB 2813 GGTCACCTCGAACCAGCCAGCGAGTCAAGACAGAGTGCAGATGCAAAACACTA 2754
 QY 121 GluAsnSerThrArgIleIleGluValLeuCysLysGluLysGluCysAsnIleAspGlu 140
 DB 2753 GAAATATATCAAGAAATATATGAAATCTCTGTAAAGAACATGATATATATGATGAG 2694
 QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluValThr 160
 DB 2693 GTGAAATGCTATGATGCAAGATTAATTTTATACCTTTATCAATTCCTTGACTGTAA 2634
 QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
 DB 2633 TCTAATGACTTCCAGAGGTTGAAATCTTCTTAAACGATACGAAGAAATTTATCTTAA 2574
 QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
 DB 2573 AATTAAGATCTAGATGCAAGATTAATTTTGTGATCATGATAAACCTTCACAGCTGATCT 2514
 QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
 DB 2513 ATTAACAGTTTGAACACAGACAGACACCAACCAAAAGTAACCTTGATGAAAGCTGAT 2454
 QY 221 ValIleProHisThrProValArgThrValMetAsnThrIleGlnLeuMetLeu 240
 DB 2453 GTAATTCCTCCACACTCCAGTTAGACTGTATGAACACATATCAACAATTAATGATG 2394
 QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAspCys 260
 DB 2393 ATTTAAATTCAGCAAGTATCAACTTCAGAAATTCGATTTCTTATTTTAAACAAGTGC 2334
 QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
 DB 2333 ACAGTGAATCCAAAGAAAGTAATATACGAAAGTCAAGATATAGATATACATCTTTAA 2274
 QY 281 GluLysPheAlaLysAlaValGluGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
 DB 2273 GAGAAATTTGCTAAAGCTGAGGACAGGGTGTGTGGAATTTGGATCCACAGGATACAAA 2214
 QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
 DB 2213 CTTGAGTCTGCTTGTATATACGAGTAATGAAATCAATCTTAATTCAGAAAGAAAGCA 2154

QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeu 340
 DB 2153 TTATCCATTTCAAAATTTTACCAAACTTCTGATGACACACTTTTTCATATGCTTTATTTG 2094
 QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
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 QY 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
 DB 2033 TCTGGAACAGATTTGCTCTTCCATGATCTGAAATCTGATATTTTAAACCTTTGAT 1974
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluValAsnLeuThrArgGluMetIle 400
 DB 1973 TTTTCAAAAGTATCGAAAGTTTATCAAAAGCAGAAAGCAACTTGACAGAGAAATGATA 1914
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
 DB 1913 AATCATTTNAGAACATGATGAAACATCGAATCATGGAATCCTTGCAATGCTCAATTC 1854
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
 DB 1853 CCTTATTTGATCTTATTAACAATCAAGACCGAAGACCAACTGATCACCTTGAA 1794
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaMetTyrLeu 460
 DB 1793 TCTGCTTCTCTTATCTTATCTTCTCCAGATTAATCACCTGACACATATGATATCT 1734
 QY 461 SerProValArgSerProLysLysGlySerThrArgValAsnSerThrAlaAsn 480
 DB 1733 TCTCTGTAAATGATCCCAAGAAAGTTCAACTACGCGTAAATTTCTACTCAAT 1674
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 DB 1673 GAGAGACACAAAGCACTCAGCTTCCAGACCGAGCATGAAATGAAATCTCTCT 1614
 QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
 DB 1613 TCACGTGTTTAAAGTAAAGTATCGCGTACCTATCTCCGCTTAATACACTGTTGAA 1554
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheThrPheGlnHisThr 540
 DB 1553 CGCCTTCTGCTGAGACACCGAATTTGAACATATCTCTGAGCCCTTTTCCAGACAC 1494
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
 DB 1493 CTGCAAGATGAGTATGAACATCATGAGAGACAGCAATTTGGACCAATTTATGATGTTCC 1434
 QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
 DB 1433 ATGTATGCGCATATGCAAAAGTCAAAATATATGACCTTAAATTCAAATTCATTTACAGCA 1374
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
 DB 1373 TACAAGATCTTCTCATGCTGTCCAGAGACATTCAAACGTGTTTGTGATCAAAAGAG 1314
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 DB 1313 GAGTATGATTTATATATATATTTCTATATCTCGCTCTTCTGAGAGACTGAAACAAAT 1254
 QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 DB 1253 ATTTTGCAAGTATGCTCCACAGGCCCTTCACTTGACACCAATATCTCACATCTCTCGA 1194
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
 DB 1193 AACCTTCAAGATTTCTAGTACCTTACGGAATTCCTGGAGGAACTCATATATTTCA 1134
 QY 661 ProLeuLysSerProTyrLysIleSerGluGluLeuProThrProThrLysMetThrPro 680
 DB 1133 CCCCTGAAGAGTCAATATAAATTTTCAAGAGGCTGCGCAACCAACCAAAATGACTCA 1074

Alignment Scores:			
pred. No.:	0	length:	3232
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-026-459A-37 (1-781) x US-08-470-091-1 (1-3232)

QY	1	MeSeSaRgLeuLeuLysLysTyRAspValLeuPheAlaLeuPheSerLysLeuGluArg	20
Db	124	ATGTCAAGACTGTGTGAAGAAAGATGATGATGTTGTGTGACCTTCTACCAAAATGGGAAAG	183
QY	21	ThcCysGluLeuLeuIleTyRLeuThrGlnProSerSerSeriLeSerThrGluIleAsnSer	40
Db	184	ACATGTGAACCTTAATATTTGACACAAACCCAGACAGTGTGATCTACTGAATAATATCT	243
QY	41	AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln	60
Db	244	GCAATTGGTCTTAAAGGTTTCTGGATCACATTTTATTAAGCTAAAGGGGAAGATTATACAA	303
QY	61	MeGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyRPhaIle	80
Db	304	ATGGAAGATGATCTGTGATTTCTATTCAAGTTAATGCTATGATGTCCTGACTATTTTAT	363
QY	81	LysLeuSerProProMetLeuLeuLysGluProTyLysTrpAlaValIleProIleAsn	100
Db	364	AAACTCTACCTCCACTGTGTGCTCAAGAACCAATTAACAGCGCTTATTAACCATTAAT	423
QY	101	GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu	120
Db	424	GGTTTCACCTCGAAGACCCAGCGCGATCGAGAACAGAGATCGACGATACGAAACAACTA	483
QY	121	GluAsnAspThrArgIleIleGlnValLeuCysGlyGlnHisGluCysAsnIleAspGlu	140
Db	484	GAATATGATACAAAGATTTATTGAAGTTCTGTGTAAAGACATGATTAATATAGATGAG	543
QY	141	ValLysAsnValTyRPhelYsAsnPhelLeProPheMetAsnSerLeuGlyLeuValThr	160
Db	544	GTGAAAAAGTTTATTTCAAAAATTTTATACCTTTATGAATCTCTGTGACATTTGACA	603
QY	161	SeSaRnGlyLeuProGluValGluAsnLeuSerLysArgTyRGlulGluIleTyRLeuLys	180
Db	604	TCTAATGCACTTCCAGAGGTGAAAAATCTTTTCAAAACGATACGAAAGAAATTTATCTTAA	663
QY	181	AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer	200
Db	664	AATTAAGATCTGAGTACGAAGATTTATTTTGTGATCATGATTAACACTCTTCAGACTGATTC	723
QY	201	ILAspSerPheGluThrGluArgThrProArgLysSerAsnLeuAspGluGluValAsn	220
Db	724	ATGGAACGTTTGGAAACACAGAGAACCCACGAAAAAGTAACTTGTATGAAAGGTGAAT	783
QY	221	ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet	240
Db	784	GTAATTCTCCACACACATCCAGTTAGACAGCTTATGAACACTATACCAACATTAATGAAG	843
QY	241	ILeLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyRPhaAsnAsnCys	260
Db	844	ATTTAAATTCAGCAAGATGACAACTTCGAAAAATCTGATTTCTCTATTTTAACAACTGC	903
QY	261	ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyRILEPheLys	280
Db	904	ACAGTAAATCCAAAAGAAAGATATCTGAAAAGAGTGAAGATATAGGATACATCTTTAA	963
QY	281	GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyRlys	300
Db	964	GAAATTTTTCGTAAGCTGTGGGACAGGGTTGTGTGAAATTTGGATCACAGCATACAA	1022
QY	301	LeuGlyValArgLeuTyRArgValMetGluSerMetLeuLysSerGluGluGluArg	320

Db 1024 CTGGAGTTCGCTTGTATACCGAGTAATGAAATCCATGCTTAATTCAGAGAAAGACGA 1083
 Qy 321 LeuSer11eGlnAsnPhseSerLysLeuLeuAsnAspAsn11ePheH1sMetSerLeuLeu 340
 Db 1084 TTATCCATTCAGAAATTTTACCAACCTTCGATGACACATTTTTCATATGCTTTATNTG 1143
 Qy 341 AlaGlyAlaLeuGluValValMetLalaThrThySerArgSerThrSerGlnAsnLeuAsp 360
 Db 1144 GCGTGGGCTGTGAGGTGTATATGCGCAATATGACAGAAATGACATGACAGAAATCTGGAT 1203
 Qy 361 SerGlyThrAspLeuSerPheProTrp11eLeuAsnVal11eAsnLeuLysAlaPheAsp 380
 Db 1204 TCTGGAAACGATTTCTCTTCCATGATTCGAAATGCTTAATTTAAAGCCCTTGAT 1263
 Qy 381 PheTyLysVal11eGlnSerPhe11eLysAlaGlu1YAsnLeuThrArgGluMetL1e 400
 Db 1264 TTTTACAAAGTCATGGAAGTTTATTCAAAGCAGAAAGCAGACTTGACAAAGAAATGATA 1323
 Qy 401 LysHisLeuGluArgCysGlnHisArg11eMetGluSerLeuAlaTrpLeuSerAspSer 420
 Db 1324 AAACATTTTGAACGATGTGAACATGCAATCATGGAATCCCTTGCATGAGCTCTCAGATTTCA 1383
 Qy 421 ProLeuPheAspLeu11eLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
 Db 1384 CCTTATTTGATCTTATTAACAATCAAAAGACCGAAGAACCAACTGATCACCCTTGA 1443
 Qy 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetCysTrpLeu 460
 Db 1444 TCTGCTTTCCTCTTAACTCTTCTCCAGATATATACACACGACGACATATGATCTT 1503
 Qy 461 SerProValArgSerProLysLysLysGlySerThrArgValAsnSerThrAlaAsn 480
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 Qy 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 Db 1564 GCAGAGACACAGCAACCTCAGCTCCAGACCCAGAACGATGAAATCTACCTCTT 1623
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 Db 1624 TCACTTTTATTAATAAAGTATATCGGCTATCGGCTATTCGCGGTAAATACACTTTTGCA 1683
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 Db 1744 CTGCAGAAATGATGAACTCATGAGAGACAGGCAATTGGACCAATTAATGATGTGTTCC 1803
 Qy 561 MetTyGly11eCysLysValLysAsn11eAspLeuLysPheLys11eLeuValThrAla 580
 Db 1804 ATGTATGSCATATGCAAAAGTAAAGAAATATGACCTTAATTCAAATTCATGTAACAGCA 1863
 Qy 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeu11eLysGlnGlu 600
 Db 1864 TACAAGAGATCTCTCATGCTGTTGACAGAGACATTCAAACGCTGTTTGCATCAAGAAAG 1923
 Qy 601 GluTyAspSer11eValPheTyAsnSerValPheMetGlnArgLeuLysThrAsn 620
 Db 1924 GAGTATGATCTATATATGATCTATATATCTGCTTCATGAGAGACTGAAACAAAT 1983
 Qy 621 11eLeuGlnTyAlaSerThrArgProProThrLeuSerPro11eProHis11eProArg 640
 Db 1984 ATTTTGCATATGCTTCCACAGGCCCTTACCTTGTACCAATATACCTACATTCCTGCA 2043
 Qy 641 SerProTyLysPheProSerSerProLeuArg11eProGly1YAsn11eTyTrLieser 660
 Db 2044 AGCCCTTACAAAGTTTCCAGATCCCTTACGAGATTCCTGAGAGCAACATCTATATTCA 2103
 Qy 661 ProLeuLysSerProTyLys11eSerGluGlyLeuMetProThrProThrLysMetThrPro 680
 Db 2104 CCGCTGAAGTCCATATTAATTTTCAGAAAGTCTGCCAAACCAACAAATATGCTCA 2163

Qy 681 ArgSerArg11eLeuValSer11eGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
 Db 2164 AGATCAAGATCTCTGATATCATATTTGTAATCATTCGGGACTTCTGAGAGTCCAGAAA 2223
 Qy 701 11eAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerLysGlnGly1YSerAsn 720
 Db 2224 ATTAATCAATGATGTATATACAGGACCGCTGTCTCAAAAGAGTGTCTGAGAGAGAAC 2283
 Qy 721 ProProLysProLeuLysLysLeuArgPheAsp11eGluGlySerAspGluAlaAspGly 740
 Db 2284 CCGCTTAAACCACTGAAAAAATCAGCTTGAATGTAAGATGACAGATGAGCAGATGGA 2343
 Qy 741 SerLysHisLeuProGly1YLysSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 Db 2344 AGTAAACATCTCCAGAGAGATCCCAATTTTCAGCAGAAACTGGCAAAATGACTTCTACT 2403
 Qy 761 ArgThrArgMetGlnLysGlnLysMetLysAspSerMetLysPThrSerAsnLysGluGlu 780
 Db 2404 CGAACCGAATGCAAAACGACGAAATGAAATGATGATGATGATCTCAAAACAAAGAGAG 2463
 Qy 781 Lys 781
 Db 2464 AAA 2466

RESULT 9
 US-08-470-091-2/c
 Sequence 2, Application US/08470091
 Patent No. 5912236

GENERAL INFORMATION:
 APPLICANT: Xu, Hong-Ji
 APPLICANT: Hu, Shi-Xue
 TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
 TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,091
 FILING DATE: JUN-16-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/038,760
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Poissant, Brian M
 REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 7409-025-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 941-8690
 TELEFAX: (212) 869-9741/8664
 TELETYPE: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3232 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: not relevant
 MOLECULE TYPE: DNA
 US-08-470-091-2

Alignment Scores:

Pred. No.: 0 Length: 3232
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 100.008 Indels: 0
 DB: 2 Gaps: 0

US-09-026-459a-37 (1-781) x US-08-470-091-2 (1-3232)

QY 1 MetSerArgLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
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 Db 3113 ATGTCAAGACTGTGAAGAGATGATGATGTTGCTTGACCTTGACCAAAATGGAAG 3054
 |||||
 QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerLysSerThrGluIleAsnSer 40
 |||||
 Db 3053 ACATGTGACTTATATATATGACACACCCAGGAGTTCATCTACTGAAATTAATTC 2994
 |||||
 QY 41 AlaLeuValLeuLysValSerTrpIleThrPheLeuAlaLysGlyValLeuGln 60
 |||||
 Db 2993 GCATTGGTGCTAAAGATTCTTGATCACCATTATTATGCTMAAGGGGAGATTTACA 2934
 |||||
 QY 61 MetGluAspSerLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
 |||||
 Db 2933 ATGGAAGATGATCTGGTATTCATTGATGATTAATGCTATGTCCTGACTATTTAT 2874
 |||||
 QY 81 LysLeuSerProPheMetLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
 |||||
 Db 2873 AATCTGTCACTCCATGTTGCTCAAGAACCTATTAACACGCTGTTATACCATTAAT 2814
 |||||
 QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
 |||||
 Db 2813 GGTTCACTCCGACACCCAGGCGAGTCAAGACAGAGTGCAGGATGCAAAAACAATA 2754
 |||||
 QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
 |||||
 Db 2753 GAAATAGATACAAAGATATGTAAGTCTCTGTAAAGAACATGAATATATGATGAG 2694
 |||||
 QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluValThr 160
 |||||
 Db 2693 GTGAAAATGTTTATTTTCAAAATTTTATACCTTTTATGAAATTCCTTGACCTGTACA 2634
 |||||
 QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
 |||||
 Db 2633 TCTTAAGGACTCCAGAGTGTGAAAATCTTTTAAACGATACAGAAATTTATCTTAA 2574
 |||||
 QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
 |||||
 Db 2573 AATTAAGATCTGATGATGCAAGATATTTTGTGATCATGATTAACCTTCACAGCTGATTC 2514
 |||||
 QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
 |||||
 Db 2513 ATAGACAGTTTGAACACACACACACACACGAAAGATTAACCTTGATGAGAGGTGAAT 2454
 |||||
 QY 221 ValIleProIleThrProValArgThrValMetAsnThrIleGlnGlnLeuMet 240
 |||||
 Db 2453 GTAAATCCCTCCACACACACACACAGTGTATGAAACATCAATCAAAATTAATATG 2394
 |||||
 QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAspCys 260
 |||||
 Db 2393 ATTTTAATTTGCAAGAGTATCAACTCTTGAGAAATCTGATTTCTATTTTAACAACCTGC 2334
 |||||
 QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
 |||||
 Db 2333 ACAGTGAAATCCAAAGAAAGATATGCAAGAAAGATGAAAGATATAGATATATCTTTAAA 2274
 |||||
 QY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
 |||||
 Db 2273 GAAATAATTTGCTAAAGCTGTGGACAGGGTGTGCTGAAATGGATGATCAGCAGATACAAA 2214
 |||||
 QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
 |||||
 Db 2213 CTGGAGTTCGCTGTATATACGAGTATGGAATCATCTTAATTCAGAAAGAAAGACGA 2154

QY 321 LeuSerIleGlnAsnPheSerLysLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
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 Db 2153 TTATCATTTCAAAATTTTACCAACATCTTGAAATGCAACATTTTCTATATGCTTATATG 2094
 |||||
 QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
 |||||
 Db 2093 GCGTGCCTCTTGAGGTGTGAATGGCCACATATACCAAAATCATCTCGAAATCTTGAT 2034
 |||||
 QY 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValIleAsnLeuLysAlaPheAsp 380
 |||||
 Db 2033 TCTGGAAACAGATTTGTTCTTCCATGATTTGATGATGCTTAATTTAAAGCCTTGAT 1974
 |||||
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluLysAsnLeuThrArgGluMetIle 400
 |||||
 Db 1973 TTTTACAAAGATCGAAATTTTATCAACAGCAAGCACTTGACAAAGAAAGATA 1914
 |||||
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
 |||||
 Db 1913 AATCATTTAAGAACGATGTGAACATCGAATCATGGAATCCCTTGATGCTCAGATTCGA 1854
 |||||
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGln 440
 |||||
 Db 1853 CCTTATTTGATCTTATTAACAATCAAGAGACCGAAGAGCACTGATGACTTGAA 1794
 |||||
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
 |||||
 Db 1793 TCTGCTTGTCTTATCTTCTCTCCAGAAATATATCACTGACGACGATATGATCTT 1734
 |||||
 QY 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
 |||||
 Db 1733 TCTCTGTAAATCTCCAAAGAAAGGTTCAACATGACGCTGTAAATTTCTATCTGAAT 1674
 |||||
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 |||||
 Db 1673 GCAGAGACACAAGACACCTCAGCTTCACAGCCAGAACCATGAAATGTACTCTCTT 1614
 |||||
 QY 501 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuAlaGluAsnThrLeuCysGlu 520
 |||||
 Db 1613 TCAAGCTTTTAAAGAGTATCGGCTACGCTATCCCGCTAAATATACCTTTGTGA 1554
 |||||
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheLeuPheGlnHisThr 540
 |||||
 Db 1553 GCGCTTGTCTGTGACACCCAGAAATTAAGAACATATATCATCTGACCTTTCACGACAC 1494
 |||||
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
 |||||
 Db 1493 CTGCAGAAATGAGTATGAACATCATGACAGACAGCATTTTGACCAAAATTAATGATGTCTC 1434
 |||||
 QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValIThrAla 580
 |||||
 Db 1433 ATGTATGGCATATGCAAGAGTAAAGATATAGACTTTAAATTCAAAATCATTTGAAACGCA 1374
 |||||
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
 |||||
 Db 1373 TACAAAGATCTTCTCATGCTGTGAGGAGACATTCAAACGTGTTTGATCAAAAGAG 1314
 |||||
 QY 601 GluTyrAspSerIleIleValIlePheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 |||||
 Db 1313 GAGTATGATTTGATATATGATATCTATTAACCTGGCTTCATGACAGAGACGAAACAAAT 1254
 |||||
 QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 |||||
 Db 1253 ATTTTGCAGTATGCTTCACACAGGCCCTTACCTTGATCAACAAATCATCTCATCTCTCA 1194
 |||||
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyCysAsnIleTyrIleSer 660
 |||||
 Db 1193 ACCCTTCAAGATTTCTTACTGATCACCCTTACGAAATCTCTGAGGGAACATCTTATTTCA 1134
 |||||
 QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
 |||||
 Db 1133 CCCCTGAAGAGTCCATATAAATTTTCAGAAAGTCTGCCAACACCAACAAAAATGACTCCA 1074
 |||||
 QY 681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700

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Db      1073 AGATCAAGATCTGTATCAATTCGTAATTCCTGCGACTTGTGAAGTTCACAGAA 1014
OY      1013 ATAAATCATATGTATGTATACAGCAGCTGTGCTCAAAAGATGCTGAAGAGAGAAC 954
OY      721  PROPOLYSPROLEULYSLYSLEULARGPHEASPILEGUIGLYSERASPGUUAIAASPGLY 740
Db      953  CCTCCTAAACCACTGAAAAAACTACGCTTGTATGTGAAGATCAAGATGAAGCAGATGGA 894
OY      741  SerLysHisLeuProGlyIuSerLysPheGlnGlnLysLeuAlaGlnMetThrSerThr 760
Db      893  AGTAACATCTCCAGAGAGAGTCCAAATTCACGAGAACTGCGAAGAAATGACTTCTACT 834
OY      761  ArgThrArgMetGlnLysGlnLysMetLysAspSerMetLysThrSerAsnLysGlnLys 780
Db      833  CGAACACGATGCAAAAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 774
OY      781  Lys 781
      773 AAA 771

RESULT 10
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
; TITLE OF INVENTION: Susceptibility Gene Product
; NUMBER OF SEQUENCES: 3
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10357
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,108
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: FP-UC 1117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 139..2923
; PCT-US94-10357-1

Alignment Scores:
Pred. No.: 0
Score: 4014.00
Percent Similarity: 100.00%
Length: 2994
Matches: 780
Conservative: 1

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Best Local Similarity: 99.878
Query Match: 99.93%
DB: 5
Gaps: 0
Mismatches: 0
Indels: 0

US-09-026-459a-37 (1-781) x PCT-US94-10357-1 (1-2994)
OY      1  MetSerArgLeuLeuLysLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGlnArg 20
Db      580  ATGTCAAGACGTGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 639
OY      21  ThrCysGlnLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
Db      640  ACATGTGACTATATATTTTACACCAACCCAGAGTGCATATCTACAGCAATAATATCT 699
OY      41  AlaLeuValLeuLysValSerThrPheLeuLeuAlaLysGlnLysGlnLysGlnLys 60
Db      700  GCATTGGCTGCTAAAGTTCTTGTGATCACAATTTTATGCTAAAGGGAAGTATTAACA 759
OY      61  MetGlnAspAspLeuValLysSerPheGlnLeuMetLysCysValLeuAspTyrPheLys 80
Db      760  ATGGAAGATGATCGTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 819
OY      81  LysLeuSerProProMetLeuLeuLysGlnProTyrLysThrAlaValLysProLys 100
Db      820  AAACCTCACCTCCCATGTTGCTCAAGAAACCATATTAACAGCTGTTATACCCATTAAT 879
OY      101  GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgLysAlaLysGlnLeu 120
Db      880  GGTTCACCTCGAACACCCAGCGAGTCAAGACAGAGAGTGCAGGATGACAAACAACTA 939
OY      121  GlnAsnAspThrArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 140
Db      940  GAAATGATACCAAGAAATATGAAAGTCTCTGTAAGAAACAAAGAAATGAAATATGATAG 999
OY      141  ValLysAsnValTyrPheLysAsnPheLysPheMetLysSerLeuGlnLysValThr 160
Db      1000  GTGAAAAATGTTATTTTCAAAATTTTATACCTTTTATACCTTTTATACCTTTTATAC 1059
OY      161  SerAsnGlyLeuProGlnValLysAsnLeuSerLysArgTyrGlnLysLysLysLys 180
Db      1060  TCTATATGACTTCCAGAGAGTGTGAAGAACTTTCTAAACGATGAGAAATTTATCTTAA 1119
OY      181  AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db      1120  AATAAAGATCTAGATGCAAGATTTATTTTGTGATCATGATTAACCTCTCAGACTATCT 1179
OY      201  IleAspSerPheGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 220
Db      1180  ATAGACAGTTTGTGAACACAGACAGAACACACGAAAGATTAACCTTGATGAAAGCTGAAT 1239
OY      221  ValIleProProHisThrProValArgThrValMetAsnThrLysGlnLysLeuMet 240
Db      1240  GTAATTCCTCCACACACTCCAGTTAGACGTGTATATACACATCTCCACAAATTAATGATG 1299
OY      241  IleLeuAsnSerAlaSerAspGlnProSerGlnAsnLeuLysSerThrPheAsnAsnCys 260
Db      1300  ATTTTAATTCAGCAGATGATCAACCTTCAGAAATCTATTTCTATTTTAAACACGC 1359
OY      261  ThrValAsnProLysGlnSerLysLysLysLysLysLysLysLysLysLysLysLysLys 280
Db      1360  ACAGTGAATCCAAAGAAAGATATATCTAAAGAGTAAAGATATATAGATATATCTTTAAA 1419
OY      281  GlnLysPheAlaLysAlaValLysGlnLysCysValGlnLysSerGlnArgTyrLys 300
Db      1420  GAGAAATTTGCTAAAGCTGTGGACAGAGTGTGTGAAATTTGATCAACAGCATACAA 1479
OY      301  LeuGlyValArgLeuTyrTyrArgValMetGlnSerMetLysSerGlnLysLysLys 320
Db      1480  CTGGAGTTCCTCTGTATTTACCAAGTAAATGAAATCCATGCTTAAATCAGAAAGACGA 1539
OY      321  LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnLysPheHisMetSerLeuLeu 340
Db      1540  TTATCCATTCAAAAATTTTACCAAACTTCTGAATGACACAACTTTTTCATATGCTTAT 1599

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QY 341 AlaCysAlaLeuGluValIValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuasp 360
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 Db 1600 GCGTCCGCTCTTGAGGTTGTAATGGCCACATATGACGAAGTCAATCTGAAATCTTGAT 1659
 QY 361 SerGlyThrAspLeuSerPheProTrrPIleLeuAsnValLeuAsnLeuLysAlaPheasp 380
 |||||
 Db 1660 TCTGGACAGATTTCTCTTCCATGGATTCGAATGTGCTTAAATTAACCCCTTGAT 1719
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
 |||||
 Db 1720 TTTTCAAAAGTATCGAAAGTTTATCAAGACGAAGGCACTTGCAAGAAATGATA 1779
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrrPheuSerAsper 420
 |||||
 Db 1780 AAACATTTTGAAGCATGTGAACATCGAATCATGGAAATCCCTTGCAAGGCTCTCAATCA 1839
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
 |||||
 Db 1840 CCTTATTTGATCTTATTAACAATCAAGACCGAAGACCAATCATCCTTGAA 1899
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTrrLeu 460
 |||||
 Db 1900 TCTGCTTCTCCCTTAATCTTCCCTCCAGAAATCAACACACGACAGATATGATCTT 1959
 QY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
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 Db 1960 TCTCTCTGAATCTCCAAAGAAAAAGTTCAACTACGCTGTAATTTCTACTGCAAT 2019
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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 Db 2020 CGAGAGACAAAGCAACCTCGCCCTCCAGACCAAGCAATGCAATCTACTCTCTT 2079
 QY 501 SerLeuPheTrrLysLysValTrrArgLeuAlaTrrLeuArgLeuAsnThrLeuLysGlu 520
 |||||
 Db 2080 TCACGTTTAAAAAGTGTATCGGCTAGCCTATCTCGGCTAAATACATTTTGTA 2139
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrrThrLeuPheGlnHisThr 540
 |||||
 Db 2140 CGCCTTCTGTGAGCACCAAGAAATAGAACATATCATCTGACCCCTTTCCAGCACACC 2199
 QY 541 LeuGlnAsnGluTrrGluLeuMetArgAspArgHisLeuAspGlnIleMetLeuTrrSer 560
 |||||
 Db 2200 CTGCGAATGAGTATGAACATCATGAGACAGGCAATTTGGACCAATTTGATGTGTTCC 2259
 QY 561 MetTrrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
 |||||
 Db 2260 ATGTATGGCATATGCAAGTGAAGAAATATGACCTTAAATTCAAAATCATTTGACACGA 2319
 QY 581 TrrLysAspLeuProHisAlaValIleGluThrPheLysArgValLeuIleLysGluGlu 600
 |||||
 Db 2320 TACAAAGATCTTCTCATGCTGTTCAAGAGACATTCMAAGCTTTTGTGTAAGAAAG 2379
 QY 601 GluTrrAspSerIleIleValPheTrrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 |||||
 Db 2380 GAGTrrGTATCTATTATAGATATCTATTAACCTCGTCTATGAGAGACTGAACAAAT 2439
 QY 621 IleLeuGlnTrrLysSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 |||||
 Db 2440 ATTTTGGCATGCTTCCACAGGCCCCCTACTTGTCAACATACCTACTTCTCTGA 2499
 QY 641 SerProTrrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTrrLysSer 660
 |||||
 Db 2500 AGCCCTTACAGTTTCTAGTCAACCTTACGGATTCCTGAGGGAACATCTATATTCA 2559
 QY 661 ProLeuLysSerProTrrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
 |||||
 Db 2560 CCCCTGAAGAGTCCATATAAAATTTCCGAAGGTCTGCCAACACAAACAAATGACTCA 2619
 QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
 |||||
 Db 2620 AGATCAAGAATCTTATGATATCAATGATGATATTCGGGACCTTCGAGAGATTCACAGAA 2679

QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn 720
 |||||
 Db 2680 ATTAATACAGATGTGATGTAAACGAGCACCGTGTCTCAAAAAGATGCTGAAGAACAAAC 2739
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluLysSerAspGluAlaAspGly 740
 |||||
 Db 2740 CTTCTTAAACCACTGAAAAAACTACGCTTTCATATGAAAGCATACAGATGACAGATGGA 2799
 QY 741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 |||||
 Db 2800 AGTAAACATCTCCCGAGAGATCCAAATTCAGCAGAAATGCGCAGAAATGACTTACT 2859
 QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGln 780
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 Db 2860 CGAACACGAATCCAAACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2919
 QY 781 Lys 781
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 Db 2920 AAA 2922
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 RESULT 11
 US-08-328-673A-7
 ; Sequence 7, Application US/08328673A
 ; Patent No. 6210939
 ; GENERAL INFORMATION:
 ; APPLICANT: Gregory, Richard J.
 ; Willis, Ken N.
 ; Maneval, Daniel C.
 ; TITLE OF INVENTION: Recombinant Adenoviral Vector and
 ; Methods of Use
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/328,673A
 ; FILING DATE: 25-Oct-1994
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/142,669
 ; FILING DATE: 25-OCT-1993
 ; APPLICATION NUMBER: US 08/233,669
 ; FILING DATE: 26-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, Timothy S.
 ; REGISTRATION NUMBER: 35,367
 ; REFERENCE/DOCKET NUMBER: 016930-000920US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2995 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 139..2925
 ; OTHER INFORMATION: /product= "RB"
 ; /note= "retinoblastoma tumor suppressor"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 ; US-08-328-673A-7

Alignment Scores:
Pred. No.: 0 Length: 2995
Score: 4007.00 Matches: 780
Percent Similarity: 99.87% Conservative: 0
Best Local Similarity: 99.87% Mismatches: 1
Query Match: 99.75% Indels: 0
Gaps: 4
DB: 4

US-09-026-459a-37 (1-781) x US-08-328-673a-7 (1-2995)

Oy 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
Db 580 ATGTCAAGACGTGTCAAAAGATGATGATGTTGTCACCTTCACCAATTTGGAAGG 639

Oy 21 ThrCysGluLeuIleTyrLeuThgInProSerSerSerLysSerThgIleAsnSer 40
Db 640 ACATGTGACTATATATTTGACACACCCAGCTGCAATCTCTGCAATTAATTCCT 699

Oy 41 AlaLeuValLeuLysValSerThrPIleThrPheLeuAlaLysGlyGluValLeuGln 60
Db 700 GCATTTGTCCTAAAGTTTCTTGATCACAATTTTATTAAGCTAAAGGGAGATTTACA 759

Oy 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
Db 760 ATGGAAGATGATCTGTGATTTCAATTCAGTAAATGCTATGTGCTTGACTATTTTAT 819

Oy 81 LysLeuSerProPheMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db 820 AAACCTCACACCTCCATGTGCTCAAAAGAACATATAAAACAGCTGTATATACCATTAT 879

Oy 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db 880 GGTTCACTCGAACACCCAGCGAGTCAAGAGAGATGACGAGATAGCAAAACACTA 939

Oy 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGlyCysAsnIleAspGlu 140
Db 940 GAAATCATATCAAGAAATTTATGAGTCTCTGTAAGAAACATGAAATATATAGTAGAG 999

Oy 141 ValLysAsnValTyrPheLysAspPheIleProPheMetAsnSerLeuGlyLeuValIle 160
Db 1000 GTGAAAATGTTATTTTCAAAAATTTATACCTTTATATGATCTCTGCACTGTAGACA 1059

Oy 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
Db 1060 TCTAATGGACTTCAGAGAGTGAATACTTTCAACGATACGAAAGAAATTTATCTTAA 1119

Oy 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db 1120 AATTAAGATCTAGATGCAAGATTAATTTTGTGATCATGATAAACCTTCAGACTGATCT 1179

Oy 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
Db 1180 ATAGACGTTTGGAAACACAGAGAACACACGAAAGAAATGAACTTGTAGTAAAGGTGAT 1239

Oy 221 ValIleProIleHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetCys 240
Db 1240 GTATTCTTCCACACACTCCAGCTTAGAGACTTATTAACATACATCAACATTAATGATG 1299

Oy 241 IleLeuAspSerLysSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
Db 1300 ATTTTAATTTACAGCATGATATCACTTCAGAAATCTGATATTCCTATTTTAACACTGC 1359

Oy 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db 1360 ACAGTGAATCCAAAAGAAAGATATCTGATAAAGAGATATAGATATCACTTTTAA 1419

Oy 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db 1420 GAGAAATTTCTTAAAGCTGTGGGACAGGTTGTGTAATGATGATCAACGACATCAAA 1479

Oy 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320

Db 1480 CTTGGAGTTCGCTTCTATACCGAGTAATGGAATTCATGCTTAATACAGAGAAAGACA 1539

Oy 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db 1540 TTATTCATTTCAAAATTTTATACCAAACTTCGAAATGACAACTTTTATATATGTCTTATG 1599

Oy 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db 1600 GCGTGGCTCTTGAGTGTGTAATGGCCACATATAGCAGAAAGTACATCTCAGATCTGAT 1659

Oy 361 SerGlyThrAspLeuSerPheProThrPheLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db 1660 TCTGGACAGATTTGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1719

Oy 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluLysLeuThrArgGluMetIle 400
Db 1720 TTTTCAAAAGTATCGAAATTTATTCAAAGCAGAGCAACTTGCAAGAAATATGATA 1779

Oy 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaThrLeuSerAspSer 420
Db 1780 AAACATTTTGAACATGATGACATGACATGACATGACATGACATGACATGACATGAC 1839

Oy 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGluProThrAspHisLeuGlu 440
Db 1840 CCTTATTTTGAATCTTATTAACATCAAGACCGAGAGACCAACATGATCCTTCAA 1899

Oy 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAspMetTyrLeu 460
Db 1900 TCTGCTTGGCTCTTATCTCTCCAGAAATATACACTGACACATATGATCTT 1959

Oy 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db 1960 TCTCCTGTAGATCTCCAAAGAAAAAGTTCACTACAGCGTGAATTTCTCTCAAAAT 2019

Oy 481 AlaIleThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db 2020 GCAGACACAAAGCAACCTCAGCTTCAGAGCCAGAGAGCATGAAATCTACCTCTCT 2079

Oy 501 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGluGlu 520
Db 2080 TCACTTTTATTAATAAAAGTATGCGGTACGCTATCCCGGCTAATATCACTTTGTGAA 2139

Oy 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheLeuPheGlnHisThr 540
Db 2140 CGCCTTCTGTGAGACCCAGAAATTAACAATATCATCTGAGACCTTTTCCAGCACACC 2199

Oy 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetLeuCysSer 560
Db 2200 CTCAGAAATGAATATGAACATCATGAGAGACAGGCAATTTGGACCAAAATATGATGTG 2259

Oy 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db 2260 ATGTATGGCATATGCAAGATGAAGAAATATAGACTTAAATTCAAATTCATTTACACCA 2319

Oy 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
Db 2320 TACAAGATCTTCCTCAGTGGCTTCAAGAGACATCAAAAGCTGTTTGAATCAAGAGAG 2379

Oy 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db 2380 GAGTATGATTCATATATATATCTATTAACCTGCTTCATGACGAGACATGAAACAAAT 2439

Oy 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db 2440 ATTTTGAATGATGCTTCCACAGGCCCCCTACCTGTGACAAATACATACATCTCTCGA 2499

Oy 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysnIleTyrIleSer 660
Db 2500 AGCCCTTACAAATTTCCATAGTTCACCCCTTACGAAATCTCGAGGAAACATCTATTTTCA 2559

Oy 661 ProLeuLysSerProTyrLysIleSerGluGluLysLeuProThrProThrLysMetThrPro 680
Db 2560 CCCCAGAAAGTCCATATTAATAATTTAGAAAGTCTGCCAACACCAACAAAAATGACTCCA 2619

2000

Db	343	-----ATCATGCTGCTACTGCTGCTGAACATGCATGATGGACCTTCCTGCTGAAAGCAAAAAGCA	396
Oy	144	Val-----ThrpheIysAsnPhelIleProPheMetAsnSerLeuGlyIleuValThr	166
Db	397	ATTAAGAGACACTACTTCTTAAGCCATATATTTCCAAACACTTTTGACAGAGAAATTTTAAAA	456
Oy	161	SerAsnGlyLeuProGluIuValGluAsn-----LeuSerLysArg	177
Db	457	GGAGATAGCTCCTCGGACACTTTCACAGTTTACTGATATATACCAAAAGCATATTAAGAG	516
Oy	174	TyrGluGluIleuIleuLysAsnLysAsnLysAsnAlaIleGluPheLeuAspHisAsp	193
Db	517	TATGAAAGAGATATGCTCTAACTGTTGGTATATTTGTATGTAGAGAGATCTTTTGTG-----	567
Oy	194	LysThrLeuGluIthrAspSerIleAspSerPheGluThrGlnArgThrProArgLys---	212
Db	568	-----CGACACAGCCACAGAGAGAAATGGAAACACCTCGAAATTC	609
Oy	213	-----SerAsnLeuAspGluIuValAsnVal-----IlePro	223
Db	610	ACTGCTGACACCCCACTTATGGGAACCTGACACACAGCGTATGTGGAGTATTAACCTTCAA	669
Oy	224	ProHis-----	225
Db	670	CAGCACTTTGAAAAAAAAGGTCATTTGCACTTTCACCCCACTGACCGAGCGAGATAT	729
Oy	226	-----ThrpValArgThrValMetAsnThrIleGluGln	237
Db	730	TTCAGGAAAAAGAACAGCTCATTACTCCTGTCATCAGCACACCAAAATGTGACCGG	789
Oy	238	LeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTryphe	257
Db	790	TTCAGAGATATTGTGGCTGGTGTGAAAAAATCCAAAGTACCAACTTAATAATATTTTT	849
Oy	258	AsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyr	277
Db	850	GAATCTTGTCGCGCAATCCCTGTGGAAAACCTTTATGAAAATCTTAAAGAAATAGACAG	909
Oy	278	IlePheLysGluLysPheAlaLysAlaValGlyGln-----GlyCysValGluIle	294
Db	910	ACTTCTCTGCAACCTATATCAATCAACAGATGMAACGACAGATCTCAATAGACTTT	969
Oy	295	GlySerGlnArgTyrLysLeuGlyValArgLeuIleTyrArgValMetGluSerMetLeu	314
Db	970	GCTGTAAACAGACTTAAGCTGCGAAGATTTTGTATATATAAATCTAGACACTGTAATG	1022
Oy	315	LysSerGluGluGluValGluLeuSerIleGlnAsnPheSerLysLeuAsnAspAsnIle	334
Db	1030	GTTTCAGGAAACACGACACTTCATGAGATGACATGTCACATGCTTTTACGCAAGATATA	1089
Oy	335	PheHisMetSerLeuLeuAlaCysAlaIleuGluValValMetAlaThrLysSerArgSer	354
Db	1090	TTTATCGTCTCTTGATGAGCTGTGTTGTGAAATATGTGCTCTTTCCTATAGC-----	1144
Oy	355	ThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeu	374
Db	1144	-----TACACCGTACACTTTTCTCGATTTATGAACTTCTC	1179
Oy	375	AsnLeuLysAlaPheAspPheIleTyrLysValIleGluSerPheIleLysAlaGluLysAsn	394
Db	1180	AACCTTGACCACTTTTACTTTTAAAGCTATTTAGAGCTGTGATCCGTCACAAAGAGGGG	1233
Oy	395	LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetLeuSerLeu	414
Db	1240	CTTCACAGGAGCAATGGGAAACACCTTAACAGCATTTGAAAGAAACAGATTTTGGAGAGTTTA	1299
Oy	415	AlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArg-----	432
Db	1300	GCATGGAGTACAGATTTCTGCACGTGGAGGAGGCTCCACAGATTTCTGCAAAACAAATCTCT	1359
Oy	432	-----	432
Db	1360	ACCTGTAAAGACTGTATATTTCCCAAAATAACTTTGAAACAGAAATGAGAAATCTGCAG	1419

Best Local Similarity: 24.21% Mismatches: 305
 Query Match: 18.16% Indels: 337
 DB: 1 Gaps: 32

US-09-026-459a-37 (1-781) x US-08-832-883-1 (1-4853)

OY 3 ArgLeuLeuLysLysTyrrAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCys 22
 |||||
 DB 520 AGATTAGAAAGAAACCTTCACTGTTCTGCTGTAATTTTAAAGAAATATGAAACCATTTT 579

OY 23 GluLeuLeuTyrrLeu-----ThrGlnProSerSerSerIleSerThrGlu-- 37
 ::::|
 DB 580 CAGGACATCTTAAATACCTCAAGAGAGAACCTCGTCAGACGAGGAGGAAAGAACAG 639

OY 38 -----IleAsnSerAlaLeuValLeuLysValSerThrPheLeuPheLeu 53
 ::::|
 DB 640 CGGCGACACCCCTGCTACTGCTGTAATTTTCCATTTTGTGGGCTTTTATATATAT 699

OY 54 AlaLysGluGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeu 73
 |||||
 DB 700 GCAAAAGGTATTTCCCATGATTAAGTATGATTTGTGTCATTTATACACCTGCTGCTG 759

OY 74 CysValLeuAspTyrrPheIleLysLeuSerProPheMetLeuLysGluProTyrrLys 93
 |||||
 DB 760 TGTGCTTTGACTTATGTT-----TATGGA 783

OY 94 ThrAlaValIleProIleAsnGly-----SerProArgThrProArgArgGly 109
 |||||
 DB 784 AATGACATCTGATTTCAATCGTAAGAACTTGTAACCTTAATTTAAAGCTTATCT 843

OY 110 GlnAsnArgSerAlaArgIleAlaLysGlnLeuGlnLysAsnPhrArgIleIleGluVal 129
 ::::|
 DB 844 GAAAGTTTTCATGTAAGATTTCAACCTTCTGTCGACCCCTGATCATTTGAGAGAA 903

OY 130 LeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal-----TyrPhe 146
 |||||
 DB 904 CTGTGCTTCCATCATGATGAGCTGTTTGGAGCAAGGAGATTAAGAACATTTCTG 963

OY 147 LysAsnPheIleProPheMet-----AsnSer 155
 |||||
 DB 964 AAACCCATATATAGCAAACTTATGAAAGAAAGCTCTTAAGGAAAGAAAGAAATCTTC 1023

OY 156 LeuGluLeuValThrSerAsnGlyLeuProGlu---ValGlnAsnLeuSerLysArgTyr 174
 |||||
 DB 1024 ACTGGGTTTCTAGAACTTGGGAACTTGGAGAGAGTTTAAAGCCATCATTAAGCCCTAT 1083

OY 175 GluGluIleTyrrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp--- 193
 |||||
 DB 1084 GAGGATATGTTTATCTGTTGGAAATTTAGATGAGCGGATATTTCTTGGAGAGATGCT 1143

OY 193 ----- 193

DB 1144 GAGGAGCAAAATTTGGACTCTCTCAAGGTCTCTCAAGCCTGTTCAGAACAGAGACTGCT 1203

OY 194 LysThrLeuGlnThrAspSerIle-----AspSerPheGluThrGlnArgThrProArg 211
 ::::|
 DB 1204 GAAAGGGGTGACGAAAGAAATCTTACACAGCATTTGACAAAGCAAGCATTTAGA 1263

OY 212 LysSerAsnLeuAspGluGluValAsnValIle-----ProProHisThrPro 227
 |||||
 DB 1264 ATCTTCACACCACTACTGCTGTTAGTACTTTAAGAGAAATAGCCCTTGTGACTCCA 1323

OY 228 ValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAsp 247
 |||||
 DB 1324 GTTCTTACAGCTACGATACCTTGAAGTCTTACACACATGCTGACAGAGCCACAGAAAT 1383

OY 248 GlnProSerGluAsnLeuIleSerTyrrPheAsnAsnCysThrValAsnProLysGluSer 267
 |||||
 DB 1384 GCACCAAGTGAAGAACTGGAACAGATTTCTCAGACATGTTCCAGAGATCCACAGGCT 1443

OY 268 IleLeuLysArgValLysAspIleGlyTyrrIlePheLysLysLysPheAla-----Lys 285
 |||||
 DB 1444 ATGTGTAACAGACATGAAAGAAATGTTGAAATATATCTCAGCATTTCCAGCCAGACGAG 1503

OY 286 AlaValGluGlnGlyCysValGluIleGlySerGlnArgTyrrLysLeuGluValArgLeu 305
 |||||
 DB 1504 GATTTCAGATTAATTTGCTTAAAGAAATTTGCCAGCAAACTATTTGTTTGGAGATGCTT 1563

OY 306 TyrTyrrArgValMetGluSerMetLeuLysSerGlnGluGlnLysLeuSerIleGlnAsn 325
 |||||
 DB 1564 TACTTAAAGTATTAAGAACTGTTATTTGACAGACAGCAAAAGAAAGCTAGGAGACATGAT 1623

OY 326 PheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGlu 345
 |||||
 DB 1624 TTATCTGGTATTCTGGAACAAAGATGATTCACAGATCTCTTGGCCTGCTGCTGAG 1683

OY 346 ValValMetAlaThrTyrrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 365
 |||||
 DB 1684 GTGCTC-----ACTTTTCTTATTAACCTTCCTGGCAAT----- 1716

OY 366 SerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrrLysValIle 385
 |||||
 DB 1717 ---TTTCCATTTATTAAGTAAATATTTGATGCTGCTCTTATCATTTTATTAAGTGATA 1773

OY 386 GluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArg 405
 |||||
 DB 1774 GAAGTATTCATTAAGCAGAGAAAGATGCGCTTGTAGAGAGGTGGTAAACACTTAATCAG 1833

OY 406 CysGlnHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeu 425
 |||||
 DB 1834 ATTTGAGAAACAGATCTTAAGATCATTTGCGATGGAACCAAGCTCCACCTGCGGAAAA 1893

OY 426 IleLysGlnSerLysAspArgGluGly-----ProThrAspHisLeu 439
 |||||
 DB 1894 ATTTGAGAACATGAAAGAAAGCTTCTTACATGTGAAGAGTCAATGCCACCTCAGAAAGCT 1953

OY 440 GluSerAla-----CysProLeuAsnLeuProLeuGlnAsnAsnHis----- 453
 |||||
 DB 1954 GAAAGGCGAGATGAATTTGATGCTGCTGCTCCCTTGTACCTCCAGAAAGGTAGTGA 2013

OY 454 -----ThrAlaAlaAsp 457
 |||||
 DB 2014 GTTCGTGCTGATTAAGAGAGCTTGAAGAGAGATTAACATCTCCAAACCATTTATGAT 2073

OY 458 MetTyrrLeuSerProValArgSerProLysLysLys----- 469
 |||||
 DB 2074 AGGTACAGCTCCACAGCAGCAGCAGCATACAGAAAGGGGCTATTTGTGAGATGATAC 2133

OY 469 ----- 469

DB 2134 CCTCTGATGAGGAGAGCGCTGGGCGCATGCCCCACAGCCCTAGTCAATGCTGTCCCT 2193

OY 470 -----GlySerThrThrArgValAsnSer----- 477
 |||||
 DB 2194 GTGCAGATGATATCTGGAGAGACTGTTCTGTCTACACAGTTCCTGAGACACTTTGATC 2253

OY 478 -----ThrAlaAsn----- 480
 |||||
 DB 2254 AACATGGCAACCGCCACTGTCTACAGCCACACATGAGGCAAGGTAACCATTTCTGTGCA 2313

OY 481 -----Ala 481
 |||||
 DB 481 ----- 481

DB 2314 GGTATTCGCAATGAATAATGAGGAGTAAATCTTCTCCCTGCTCAAGTCAATGTGGGGGG 2373

OY 482 GluThrGlnAla---ThrSerAlaPheGln----- 490
 ::::|
 DB 2374 CAGGACAAAGCTGTGACAGGCTCATCATCACCCCTCAGTCTCAGGCCCTGGCTGAAGT 2433

OY 490 ----- 490

DB 2434 CTGAGCTCTCAACAGGTGACAGAAACAATTTTGCAAGTCCCTGCTCAAGTGGCCATTCA 2493

OY 491 -----ThrGln 492
 ::::|
 DB 2494 CAGATTTCCAGAGGTGGCCAAAGCAGACAGCAAGCAAGGCCAGTCTGTAAACAGAGTATAT 2553


```
OY 94 ThrAlaValIleProIleasnely-----SerProArgThrProArgArgely 109
Db 784 AATGCACTTCAGTTCATTCGTAAGACACTGTGTAACCCATTATTTAAAGCCTTAACT 843
OY 110 GluAsnArgSerAlaArgIleAlaIleAsnIleGluAsnAspThrArgIleIleGluVal 129
Db 844 GAAATATTCATCTCAAGATTCCTAAACCTTCCTGTCGACCCCTTGATCATTTAGAA 903
OY 130 LeuGlySerGluHisGluGlyAsnIleAspIleValIleAsnVal-----ThrPhe 146
Db 904 CTGCGTTCCTTACATCATGCGCTAGTTTGGAAACCAAGCGATTAAGAACATTTCTGG 963
OY 147 LysAsnPheIleProPheMet-----AsnSer 155
Db 964 AAACCTCATATTAAGAACTTATGAAAAAAAGCTCTTAAGGAAAAAGAAATATCTC 1023
OY 156 LeuGlyLeuValThrSerAsnGlyLeuProGlu---ValGluAsnIleSerLysArgTyr 174
Db 1024 ACTGGGTTTCTAGAACCTGGAACTTGGAGAGATTATTAACCCATCAATTAAGGCTAT 1083
OY 175 GluGluIleIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp--- 193
Db 1084 GAGAGATATGTTTATCTGTGGGAATTTAATGACCGATATTTCTTGGAGAGATCTCT 1143
OY 193 ----- 193
Db 1144 GAGAGAAATTTGGACTCTCTCAAGGTCTGAAACCGTTCAGAGAACAGACTGCT 1203
OY 194 LysThrIleGluIleThrAspSerIle-----AspSerPheGluIleThrGlnArgThrProArg 211
Db 1204 GAAAGGCTGCAGATGAAAAACATCTTACAGCAGCATTTGCAACATGCAACACTTGA 1263
OY 212 LysSerAsnLeuAspGluIleValAsnValIle-----ProProHisIlePro 227
Db 1264 ATCTCCACACCACTACTGCTGTAGTACATTAAGAGAAATAGCCCTTGCTGTGACTCA 1323
OY 228 ValArgThrValMetAspThrIleGluIleGluMetIleIleLeuAsnSerLysAsp 247
Db 1324 GTTTCACACCTACGATACGTCGTGAGTGTCTTACACACCATGCTGCACAGCCTCAGAAAT 1383
OY 248 GlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSer 267
Db 1384 GCACCAAGTGAAGAACTGACACAGATTCCTCAGACATGTTCCAGAAATCCACCGACT 1443
OY 268 IleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla-----Lys 285
Db 1444 ATTCTCAACAGACTGAAGAAAGATTTGAATATATTCAGCATTTCCAGCCACAGACAG 1503
OY 286 AlaValGlyGlnGlySerValGluIleGlySerGlnArgTyrLysLeuIleValArgLeu 305
Db 1504 GATTTCAGTAAATTTGCTAAAGAAATTTCCAGCAAAATTTTCTGTTTGGCAGATGCTT 1563
OY 306 TyrTyrArgValMetGluSerMetLeuLysSerGluGluIleGluArgLeuSerIleGlnAsn 325
Db 1564 TACTATTAAGTATTAAATCTGTATTTAGCAGCAAGAAAGAAAGCTAGACATGAT 1623
OY 326 PheSerLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaSerLeu 345
Db 1624 TTATCTGTATCTGGAACAACATCATTCACAGATCTCTCTGCGCTGCTTGAAG 1683
OY 346 ValAlaMetAlaThrTyrSerArgSerThrSerGlnLeuAsnAspSerGlyThrAspLeu 365
Db 1684 CTCCTC-----ACTTTTCTTATTAAGCCTCTCGGAAT----- 1716
OY 366 SerPheProIleIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrIleValIle 385
Db 1717 ---TTTCCATTTATTTAGTAATATTTGATGCTCTTATTAATTTATTAAGGTGATA 1773
OY 386 GluSerPheIleLysAlaGluIleLysLeuThrArgLysMetIleLysHisIleGluArg 405
Db 1774 GAAATATTCATTTAGACCAAGATGCTTGTAGAGAGGTGTAAACACACTTAATCAG 1833
OY 406 CysGluHisArgIleMetGluSerLeuAlaIlePheLeuSerSerProLeuPheAspLeu 425
Db 1834 ATTTGAAGAACAGATCTTGAATCATTTTGGCATTTGAGAAACCAAGAGTCTCATCTGGGAAAA 1893
OY 426 IleLysGlnSerLysAspArgGluGly-----ProThrAspHisLeu 439
Db 1894 ATTTAGAACAAATGAAGAAAGATTCCTACATGTGAAAGAGTATGCTCCACATCAAGACTG 1953
OY 440 GluSerAla-----CysProLeuAsnIleProLeuGlnAsnHis- 453
Db 1954 GAAAGGCGAGATGAATTTGCATTGTGCGTCCCTTTTACCTCCAGAAAGGTGACTGAA 2013
OY 454 -----ThrAlaIleAsp 457
Db 2014 GTTCTGCTGATCTGAGAGACTTGGAAAGGATTAACATCTCCAAACCAATTAATGAT 2073
OY 458 MetTyrLeuSerProValArgSerProLysLysLys----- 469
Db 2074 AGGTACAGCTCCCCACAGCCAGCATACCAAGAAAGCGGCTATTGTTGAGAAATGATAGC 2133
OY 469 ----- 469
Db 2134 CCTCTGATGAGAGACCGCTGGGCGCATGCCCCCAACGCCCTAGTCAATGCTGTCCCT 2193
OY 470 -----GlySerThrThrArgValAsnSer----- 477
Db 2194 GTGCAGATATATCTGGGAGAGACTGTTTCTGTCAACACAGTTCTTGACAGACTTGGTC 2253
OY 478 -----ThrAlaAsn- 480
Db 2254 ACCATGGCAACCGCCACTGTGCACAGCCAAAGTGGCAACGTAACCATTCCTGTGCAA 2313
OY 481 -----Ala 481
Db 2314 GGATATGCCAATGAATGAAGGATTAACATTTCTCCGTCCAAATGCAATGTTGGGGG 2373
OY 482 GluThrGlnAla---ThrSerAlaPheGln----- 490
Db 2374 CAGGCACACAGCTGTGACAGGCTCATCCAGCCCTCAAGTGTCAAGCCCTGGCTGGAAAT 2433
OY 490 ----- 490
Db 2434 CTGAGCTCTCACAGGTGACAGAAACAATTGCAAGTCCCTGGTCAAGTGGCATTCAA 2493
OY 491 -----ThrGln 492
Db 2494 CAGATTTCCCGAGGTGGCCAAACAGCAGAAAGCCAGTGTGAACCAAGCATGATAAT 2553
OY 493 LysProLeuLysSerThrSerLeuSerLeuPheTyrLysValIleTyrArgLeuAlaTyr 512
Db 2554 AGACCCAGAAACACAGCTCTTATCGCTTTCTTTGAAAGATATACATTTAGCAGCT 2613
OY 513 LeuArgLeuAsnThrLeuGlyGluArgLeu---LeuSerGlnHisProGluLeuGluHis 531
Db 2614 GTCCGCTTGGGATCTGTGCGCAAACTAGATATTTACAGAT-----CAATTAAGGAAA 2667
OY 532 IleIleThrPheLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetAlaAspArg 551
Db 2668 AAAATCTGAGCCGCTGCAATCTCCATTAATTCAGTGTGCTGAACTTATGATGAGACGA 2727
OY 552 HisLeuAspGlnIleMetIleCysSerMetTyrGlyIleCysLysValIleAsnIleAsp 571
Db 2728 CATCTGACAGATTTAATGATGTGCAATTTATGTATGACCAAGGTCAACAAAGAAAT 2787
OY 572 LeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluThr 591
Db 2788 AAGTCTTCCAAACATTAATGCTGTTTATGAGACTACCGCAGGCGGAGGAGG 2847
OY 592 PheLysArgValLeuIleLys----- 598
Db 2848 TATAGAAAGTGTGATTAAGGGAAGGAAAGAAATTCGACGACGATGATACG 2907
OY 598 ----- 598
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Page 25

Db	2908	AAAGCCATCAGAAATTCCTCCAAAGAAAGAAATTAACAAAGATAGAAACCAAGTAGAGACTCAGT	2967
Qy	598	-----	598
Db	2968	CCAGTTATGAGTGCAAGAGACACCTTGGCCATTCACAGCCCAAGACAGTGCCTCCACAA	3027
Qy	599	-----glu ln l u t y a s p s e l l e l e -----	606
Db	3028	CCTACTCGCCTCAGACAGTGGCCACACAGTGCAGTGAAGAAAGAGAGAGCGGACACTCATTT	3087
Qy	607	ValPhe y t y s e r v a l Phe me G n a g l e u s t y r s n l e u e n t y -----	624
Db	3088	CAGTTCACACAAACATCTACATATAACAGATTAGACATTTGCATGATATCTCAGC	3147
Qy	625	Ala S e r t H a r g p r o t H e u s e r P o l e P o H s l e P r o a r g S e r P o t y L y s -----	644
Db	3148	GCMAATATGATGATCTCTCCACTCTCTCCCTTCATCCATTGTAAAG-----	3192
Qy	645	Phe P r o S e r S e r P r o l e u s t y r l e -----P r o G l y L y s n l e T y r l e S e r P o -----	661
Db	3193	---ACAGGCTCCCTCGCCGGAATTCAGATTCTCTCAAAATATCTCTGCTTACATTTCCCA	3249
Qy	662	I e u s S e r P o t y r L y s I e S e r G l y L e u P r o t H P r o t H y S e r T H P r o a r -----	681
Db	3250	CATTAATAT-----GAAACATGCTTCTCTCTCA	3279
Qy	682	S e r a r G l l e u s I e S e r l l e G l y L e u S e r P H e t y r S e r C u l y S e r P H e G l n y S e r l e -----	701
Db	3280	GAAAAGATTTTCTATTACTGACGACAGT-----CCTTCAAAAGACGCTAGAGAAATTT	3333
Qy	702	a n g l e t v a l y s a n S e r P a r v a l l e u s a r S e r A l a g l y S e r a n P r o -----	721
Db	3334	AAATACTATGATTA-----CGCCACAGAGAA-----	3357
Qy	722	P r o L y S P r o L e u s t y L y S e u a r g P H e a S P l l e G l y L e u S e r P L y S e r P L y a l a S e r P L y S e r -----	741
Db	3358	---ACTCTCATTAAGAAAGAGGAGATTTCTTTTGAGAGATGGAAGTAAATATCTGCGAANA	3414
Qy	742	L y S H s l e u P r o ---G l y L e u S t y r S e r P H e G l n y S e r L e u a l u e r T H S e r T H -----	760
Db	3415	AGAAATTTGGCCCAAAATATCATCTTGCCTTATTAACCGGCTCTCCAAAGATGTAGCTAATGAC	3474
Qy	761	A r g 761-----	
Db	3475	CGT3477-----	

Search completed: January 19, 2003, 05:26:11
Job time : 114.428 secs

1
2
3

1
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3

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OM nucleic - nucleic search, using sw model

Run on: January 16, 2003, 15:20:22 : Search time 63.8803 Seconds
(without alignments)
14944.909 Million cell updates/sec

Title: US-09-026-459A-36

Perfect score: 3113

Sequence: 1 GCCGTCATGTCACAGCTGT.....AAATGAGATTATGATAGT 3113

Scoring table: IDENTITY NUC

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, NA:*

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- 6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3105.4	99.8	3232	1	US-08-038-760-1
2	3105.4	99.8	3232	1	US-08-038-760-2
3	3105.4	99.8	3232	2	US-08-470-091-1
4	3105.4	99.8	3232	2	US-08-470-091-2
5	3105.4	99.8	3232	1	US-08-204-329-2
6	2415	77.6	2994	1	US-08-482-627-4
7	2415	77.6	2994	3	US-08-801-092-3
8	2415	77.6	2994	4	US-09-315-113-3
9	2413.4	77.5	2994	5	PCT-US94-10357-1
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11	2410.4	77.4	2995	4	US-08-328-673A-7
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13	68.2	2.2	3249	1	US-08-106-493A-1
14	68.2	2.2	3249	1	US-08-429-264-1
15	68.2	2.2	4853	1	US-08-832-883-1
16	68.2	2.2	4853	2	US-08-832-877-1
17	65.6	2.1	2808	2	US-08-152-721B-1
18	59	1.9	7218	1	US-08-232-463-14
19	51	1.6	3747	4	US-09-213-293D-2
20	44.6	1.4	1803	4	US-09-134-001C-799
21	44.6	1.4	15363	4	US-08-961-527-139
22	44.4	1.4	20674	4	US-09-641-638-651
23	44	1.4	19124	2	US-08-487-826B-13
24	43.8	1.4	1056	4	US-09-134-001C-1550
25	43.2	1.4	509	4	US-09-030-607-202
26	43.2	1.4	509	4	US-09-605-785-202
27	43.2	1.4	509	4	US-09-439-313-202

28	43.2	1.4	509	4	US-09-352-616A-202	Sequence 202, App
29	43.2	1.4	509	4	US-09-232-149A-202	Sequence 202, App
30	43	1.4	5852	1	US-07-867-106-2	Sequence 2, Appl1
31	42.8	1.4	615	4	US-08-998-416-186	Sequence 166, App
32	42.6	1.4	1189	1	US-08-307-591-2	Sequence 2, Appl1
33	42.6	1.4	2606	4	US-09-234-827B-3	Sequence 3, Appl1
34	42.4	1.4	1186	2	US-08-731-722-5	Sequence 36, Appl1
35	42	1.3	665	2	US-08-883-795A-36	Sequence 4, Appl1
36	42	1.3	1864	4	US-09-468-265-4	Sequence 1, Appl1
37	41.8	1.3	1679	4	US-09-306-060-1	Sequence 13, Appl1
38	41.4	1.3	19124	2	US-08-487-826B-13	Sequence 541, App
39	41.2	1.3	821	4	US-08-998-416-541	Sequence 288, App
40	41.2	1.3	837	4	US-08-998-416-288	Sequence 7, Appl1
41	41.2	1.3	2030	2	US-08-705-937-7	Sequence 287, App
42	40.6	1.3	860	4	US-08-998-416-287	Sequence 3, Appl1
43	40.6	1.3	4078	2	US-08-960-022-3	Sequence 3, Appl1
44	40.6	1.3	6265	4	US-09-129-112-3	Sequence 36, Appl1
45	40.6	1.3	12124	1	US-08-181-271A-36	

ALIGNMENTS

RESULT 1
US-08-038-760-1
Sequence 1, Application US/08038760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
NUMBER OF INVENTION: Broad-Spectrum Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,760
FILING DATE: 19930325
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-038-760-1

Query Match 99.8%; Score 3105.4; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	7	ATGCAAGACCTGTGAAACAAAGTATGAGATGTGTTGGACGCTCTGACAAATTTGGAAG	66
Dd	124	ATGCGAAGACTGTGTAAAGAAATGATGATGATGTGTGGACCTCTTGAGAAATTTGGAAAG	183
OY	67	ACATGTGAACCTTATATATTTGACACAACCCAGCAGTTGCAATATCTAGAAATAAATTC	126
Dd	184	ACATGTGAACCTTATATATTTGACACAACCCAGCAGTTGCAATATCTAGAAATAAATTC	243
OY	127	GCAATGGTCTTAAAGTTTCTTGATGATCACTTTTATAGCAAAAGGGAAGATTTACA	186
Dd	244	GCAATGGTCTTAAAGTTTCTTGATGATCACTTTTATAGCAAAAGGGAAGATTTACA	303
OY	187	ATGGAAGATGATCTGTGATTTCACTTTCAGTTATAGCTATGTGTCTTGACTATTTTAT	246
Dd	304	ATGGAAGATGATCTGTGATTTCACTTTCAGTTATAGCTATGTGTCTTGACTATTTTAT	363
OY	247	AAACCTGCACCTCCCATCTTCTCAAGAACATATAAAGACGTTATATACCATTAA	306
Dd	364	AAACCTGCACCTCCCATCTTCTCAAGAACATATATAAAGACGTTATATACCATTAA	423
OY	307	GGTTTCACCTGAAACCCAGGCGAGTCAAGACAGGAGCGACGGATATGCAAAACAAT	366
Dd	424	GGTTTCACCTGAAACCCAGGCGAGTCAAGACAGGAGCGACGGATATGCAAAACAAT	483
OY	367	GAAATGATACAAGAATTTATGAATCTCTGTAAAGAACTGAATGATATATAGTAG	426
Dd	484	GAAATGATACAAGAATTTATGAATCTCTGTAAAGAACTGAATGATATATAGTAG	543
OY	427	GTGAAAAATGTTTATTTCAAAAAATTTTATACCTTTTATGAATCTCTGACCTGTGACA	486
Dd	544	GTGAAAAATGTTTATTTCAAAAAATTTTATACCTTTTATGAATCTCTGACCTGTGACA	603
OY	487	TCTATATGACCTTCGAGAGTTGAAATCTTCTTAAACGATATGCAAGAAATTTTCTTAA	546
Dd	604	TCTATATGACCTTCGAGAGTTGAAATCTTCTTAAACGATATGCAAGAAATTTTCTTAA	663
OY	547	AATTAAGATCTAGATGCAAGATTTATTTTGGATCATGATATAAAGCTCTTCAAGCTATCT	606
Dd	664	AATTAAGATCTAGATGCAAGATTTATTTTGGATCATGATATAAAGCTCTTCAAGCTATCT	723
OY	607	ATAGACAGTTTGAACACACAGAGAACCCACGCAAAAAAGTAACTTGATGAAGAGTGAT	666
Dd	724	ATAGACAGTTTGAACACACAGAGAACCCACGCAAAAAAGTAACTTGATGAAGAGTGAT	783
OY	667	GTAATTCCTCCACACACCTCCAGTTAGAGATCTGTATGAACACTATACCAATTAATGAT	726
Dd	784	GTAATTCCTCCACACACCTCCAGTTAGAGATCTGTATGAACACTATACCAATTAATGAT	843
OY	727	ATTTTAAATTCAGCAAGTATCAACCTTCAGAAAACTGATTTTCTATTTTAAACAACCTC	786
Dd	844	ATTTTAAATTCAGCAAGTATCAACCTTCAGAAAACTGATTTTCTATTTTAAACAACCTC	903
OY	787	ACAGTAAATCCAAAAGAAATATCTGTATATAAAGAGTGAAGATATAGGATATCACTTTTAA	846
Dd	904	ACAGTAAATCCAAAAGAAATATCTGTATATAAAGAGTGAAGATATAGGATATCACTTTTAA	963
OY	847	GAGAAATTTGCTTAAAGCTGTGTGGACAGGGTGTGTCTGAAATTTGATCAACAGCATTCAAA	906
Dd	964	GAGAAATTTGCTTAAAGCTGTGTGGACAGGGTGTGTCTGAAATTTGATCAACAGCATTCAAA	1023
OY	907	CTTGAGATTCGCTTGTATTTACCGAGTATATGGAATCCATGCTTAAATCAGAAAGAACGA	966
Dd	1024	CTTGAGATTCGCTTGTATTTACCGAGTATATGGAATCCATGCTTAAATCAGAAAGAACGA	1083
OY	967	TTTATCAATTCAAAATTTTATAGCAACCTTGGAATGCAACATTTTTCATATGTCTTATATG	1026
Dd	1084	TTTATCAATTCAAAATTTTATAGCAACCTTGGAATGCAACATTTTTCATATGTCTTATATG	1143
OY	1027	GCGTGCAGCTCTTGAGGTGTATATGGCCACATATAGCAAGATACATCTCGAATCTTGAT	1086
Dd	1144	GCGTGCAGCTCTTGAGGTGTATATGGCCACATATAGCAAGATACATCTCGAATCTTGAT	1203

OY	1087	TCGGAAGAGATTTGGCTCTTCCCATGGATCTCGAATGAGCTTAATTTTAAAGCCTTGAT	1146
DB	1204	TCGGAACGATTTGTCTTCCATGGATTCGAAATGCTTAATTTAAAGCCTTGAT	1263
OY	1147	TTTTACAAAGTAGCAAAAGTTTATCAACGAGAAAGCACTTGACAAAGAAATGATA	1206
DB	1264	TTTTACAAAGTAGTGAAGAGTTTATCAACGAGAAAGCACTTGACAAAGAAATGATA	1323
OY	1207	AAACATTTAGAAGATGTGAATCATGAAATCCCTGGATGGCTCGATTTGA	1266
DB	1324	AAACATTTAGAAGATGTGAATCATGAAATCCCTGGATGGCTCGATTTGA	1383
OY	1267	CGTTTATTTGATCTTATTTAAACAATCAAAGACCGAAGACCACACTGATCCTTGAA	1326
DB	1384	CGTTTATTTGATCTTATTTAAACAATCAAAGACCGAAGACCACACTGATCCTTGAA	1443
OY	1327	TCGCTGTGCTCTTATTCCTCTCTCCAGAAATATCAACCTGACGACGATATGATCTT	1386
DB	1444	TCGCTGTGCTCTTATTCCTCTCTCCAGAAATATCAACCTGACGACGATATGATCTT	1503
OY	1387	TCCTCGTTAAGATCTCCAAABAAAAAGGTCACTACGGCTGTAATTCCTACTCGAAT	1446
DB	1504	TCCTCGTTAAGATCTCCAAABAAAAAGGTCACTACGGCTGTAATTCCTACTCGAAT	1563
OY	1447	GCAGAGACACAAAGCACTCAGCCTTCAGACCCAGAAAGCATTTGAATCTCTCTT	1506
DB	1564	GCAGAGACACAAAGCACTCAGCCTTCAGACCCAGAAAGCATTTGAATCTCTCTT	1623
OY	1507	TCACGTGTTTATAAAAAGTATCGGCTATCGGCTATCTCCGGCTAAATACCTTTGTGA	1566
DB	1624	TCACGTGTTTATAAAAAGTATCGGCTATCGGCTATCTCCGGCTAAATACCTTTGTGA	1683
OY	1567	CGCCTCTGCTGACACCCGGAATTTGAACATATCATCTGACCTTTTCAGACACAC	1626
DB	1684	CGCCTCTGCTGACACCCGGAATTTGAACATATCATCTGACCTTTTCAGACACAC	1743
OY	1627	CTGCAGATGAGTATGAACCTATGAGACAGGCAATTTGACCAATATGATGTGTTCC	1686
DB	1744	CTGCAGATGAGTATGAACCTATGAGACAGGCAATTTGACCAATATGATGTGTTCC	1803
OY	1687	ATGATATGGCATATGCAAAAGTGAAGATATAGACCTTAAATTCAAATATCATTTGACAGA	1746
DB	1804	ATGATATGGCATATGCAAAAGTGAAGATATAGACCTTAAATTCAAATATCATTTGACAGA	1863
OY	1747	TACAAGGATCTCCGACGCTGTCAGAGACATTCAAAGCTGTTTGAATCAAAAGAGG	1806
DB	1864	TACAAGGATCTCCGACGCTGTCAGAGACATTCAAAGCTGTTTGAATCAAAAGAGG	1923
OY	1867	ATTTCAGATATGCTCCACAGGCCCCCTACTGTGTACCAATATCTCATATCTCTCGA	1926
DB	1984	ATTTCAGATATGCTCCACAGGCCCCCTACTGTGTACCAATATCTCATATCTCTCGA	2043
OY	1927	AGGCCTTAAATTTCCATAGTTCACCTTTACGATTTCTCGAAGGGAACATCTATATTCA	1986
DB	2044	AGGCCTTAAATTTCCATAGTTCACCTTTACGATTTCTCGAAGGGAACATCTATATTCA	2103
OY	1987	CCCCGAAAGTCCATATATTAATTCAGAAAGTCTGCCAACACCAACAAAAATGATCTCA	2046
DB	2104	CCCCGAAAGTCCATATATTAATTCAGAAAGTCTGCCAACACCAACAAAAATGATCTCA	2163
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DB	2164	AGATCAAGAATTTGTATCAATTTGGGATCATTTCCGGACTTGTGAAAGTTCAGAAA	2223
OY	2107	ATTAATTCAGATGATATGTATACAGGACGCTGTCTCAAAGAAGTCTGTAAGAGCAAC	2166
DB	2224	ATTAATTCAGATGATATGTATACAGGACGCTGTCTCAAAGAAGTCTGTAAGAGCAAC	2283
OY	2167	CCCTCTTAACCACTGAAAAAATTCAGCTTTGTGATTTGAAGAGTACAGTGAAGCAGATGGA	2286

[illegible]

	TITLE OF INVENTION:	Methods for Tumor Suppressor Gene Therapy.
	NUMBER OF SEQUENCES:	3
	CORRESPONDENCE ADDRESS:	
	ADDRESSEE:	Pennie & Edmonds
	STREET:	1155 Avenue of the Americas
	CITY:	New York
	STATE:	New York
	COUNTRY:	U.S.A.
	ZIP:	10036-2711
	COMPUTER READABLE FORM:	
	MEDIUM TYPE:	Floppy disk
	OPERATING SYSTEM:	PC-DOS/MS-DOS
	SOFTWARE:	PatentIn Release #1.0, Version #1.25
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER:	US/08/038,760
	FILING DATE:	19930325
	CLASSIFICATION:	424
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Poisasant, Brian M
	REGISTRATION NUMBER:	28,462
	REFERENCE/DOCKET NUMBER:	7409-025-999
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	(212) 790-9090
	TELEFAX:	(212) 869-9741/8864
	TELEX:	66141 PENNIE
	INFORMATION FOR SEQ ID NO:	2:
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	3232 base pairs
	TYPE:	NUCLEIC ACID
	STRANDEDNESS:	double
	TOPOLOGY:	not relevant
	MOLECULE TYPE:	DNA
	US-08-038-760-2	
	Query Match	99.8%; Score 3105.4; DB 1; Length 3232;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 3106; Conservative	0; Mismatches 1; Indels 0; Gaps 0
OY	7	ATGTCAAGACTGTTGAAGAAGATGATGATGTTTGGACCTCTTCAGCAAAATGGAAAGC 66
Db	3113	ATGTCAAGACTGTTGAAGAAGATGATGATGTTTGGACCTCTTCAGCAAAATGGAAAGC 3054
OY	67	ACATGTACACTTATATATTTTGACACAACCACAGTGCATATCTACTGAATAATTC 126
Db	3053	ACATGTACACTTATATATTTTGACACAACCACAGTGCATATCTACTGAATAATTC 2994
OY	127	GCAATGTGTCTAAAAGTTTCTTGATCACATTTTTATTAGCTAAAGGGAAGATTAACA 186
Db	2993	GCAATGTGTCTAAAAGTTTCTTGATCACATTTTTATTAGCTAAAGGGAAGATTAACA 2934
OY	187	ATGSAAGATGATCGGCGGATTTATTCAGTTAATGCGATATGTCOCTGATATTATAT 246
Db	2933	ATGSAAGATGATCGGCGGATTTATTCAGTTAATGCGATATGTCOCTGATATTATAT 2874
OY	247	AAACTCCACTCCACGATGTCCTCAAGAACAATATAAACAGCTGTATACCATTAAT 306
Db	2873	AAACTCCACTCCACGATGTCCTCAAGAACAATATAAACAGCTGTATACCATTAAT 2814
OY	307	GATTCACTGACACACCCAGGCGAGGTCAAGACAGAGTGCACGGATAGCAAAACAATA 366
Db	2813	GATTCACTGACACACCCAGGCGAGGTCAAGACAGAGTGCACGGATAGCAAAACAATA 2754
OY	367	GAATATGATTAACAAGATTAATTTGAAGTTCCTGTAAAGAACATGAATTAATATGATG 426
Db	2753	GAATATGATTAACAAGATTAATTTGAAGTTCCTGTAAAGAACATGAATTAATATGATG 2654
OY	427	GTGAAAAATGTTTATTTCAAAAAATTTTATACCTTTTATGAAATTCCTTGAAGCTGTAA 486
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OY	487	TCTATGACACTTCAGAGTTGAANAATCTTCTAAACGATACGAGAAATTAATCTTAAA 546

Db 2633 TCTATGACTCTCCAGAGCTGGAAAATCTTCTTAACGATACGAGAAATTTATCTTAA 2574
QY 547 AATAAAGATCTAGATGCAAGATTTATTTTGGATCATGATATAAAGCTCTTCAGACTGATTC 606
Db 2573 AATAAAGATCTAGATGCAAGATTTATTTTGGATCATGATATAAAGCTCTTCAGACTGATTC 2514
QY 607 ATAGACAGTTTGGAAACACAGAAACACAGAAACAAATTAACCTTGATGAAGAGTGAAT 666
Db 2513 ATAGACAGTTTGGAAACACAGAAACACAGAAACAAATTAACCTTGATGAAGAGTGAAT 2454
QY 667 GTAAATCTCCACACACTCCAGTTAGACTGTATGAACACTATCCAACTTAATGATG 726
Db 2453 GTAAATCTCCACACACTCCAGTTAGACTGTATGAACACTATCCAACTTAATGATG 2394
QY 727 ATTTTAAATTCAGACAGTATCAACCTTCAGAAAATCTGATTTTCTATTTTAAACACTGC 786
Db 2393 ATTTTAAATTCAGACAGTATCAACCTTCAGAAAATCTGATTTTCTATTTTAAACACTGC 2334
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Db 2333 ACAGGATCCAAAAGAAAGTATCTGAAAAGATGAAAGTATAGATACATCTTTAA 2274
QY 847 GAGAAATTTGCTAAAGCTGTGGACAGGGTGTGTGCAAAATTTGATCAGACGATACAA 906
Db 2273 GAGAAATTTGCTAAAGCTGTGGACAGGGTGTGTGCAAAATTTGATCAGACGATACAA 2214
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QY 967 TTATCCATTCAAAATTTTAGCAAACTCTGAATGACAACTTTTCTATGCTTTATG 1026
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QY 1027 GCGTGGCCTCTTGAAGTTGTAATGCGCACATATAGCAAGATACATCTGAAATCTTGAT 1086
Db 2093 GCGTGGCCTCTTGAAGTTGTAATGCGCACATATAGCAAGATACATCTGAAATCTTGAT 2034
QY 1087 TCTGGAACAGATTTGCTTCTTCCCATGATTCGTAATGCTTAATTTAAAGCCTTTGAT 1146
Db 2033 TCTGGAACAGATTTGCTTCTTCCCATGATTCGTAATGCTTAATTTAAAGCCTTTGAT 1974
QY 1147 TTTTACAAAGTATCGAAAATTTTATCAAGACGAAAGCAATGTAACAGAAATGATA 1206
Db 1973 TTTTACAAAGTATCGAAAATTTTATCAAGACGAAAGCAATGTAACAGAAATGATA 1914
QY 1207 AAACATTTAGACGATGTAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
Db 1913 AAACATTTAGACGATGTAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1854
QY 1267 CTTTTATTTGATCTTATTAACAATCAAAGACCGAAGAGCAACTGATCACTTGAA 1326
Db 1853 CTTTTATTTGATCTTATTAACAATCAAAGACCGAAGAGCAACTGATCACTTGAA 1794
QY 1327 TCTGCTGTCTCTTAAATCTCTCTCCAGATTAATCAACCTCCAGACAGATATGATCTT 1386
Db 1793 TCTGCTGTCTCTTAAATCTCTCTCCAGATTAATCAACCTCCAGACAGATATGATCTT 1734
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QY 1447 GCAGAGACACAAGACCTCCAGCTCCAGACCCAGAACGCAATGAAATCTACTCTCTT 1506
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QY 1507 TCACTGTTTTTAAAAAGTATCGGCTAGCCTATCTCCGGCTAATACACTTTGTGA 1566
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QY 1567 CGCCTTCTGTCTGAGACCCAGAAATTAAGAAATATCATGTGACCCCTTTCCAGACACC 1626
Db 1553 CGCCTTCTGTCTGAGACCCAGAAATTAAGAAATATCATGTGACCCCTTTCCAGACACC 1494

QY 1627 CTGACAGATGATGTAAGTCAATCATAGAGACAGGCAATTTGGACCAATTAATGATGCTTCC 1686
Db 1493 CTGACAGATGATGTAAGTCAATCATAGAGACAGGCAATTTGGACCAATTAATGATGCTTCC 1434
QY 1687 ATGTATGCAATATGCAAAAGTGAAGAAATATAGACCTTAAATTCAMAATCATTTAAGCA 1746
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Db 1373 TACAAGATCTTCCATGATGCTGTTCCAGAGACATTTCAACCGTGTGATCAAAAGAG 1314
QY 1807 GAGTATGATCTTAAATTAATCTTAACTGGCTTCAATGACAGAGACTGAAAACAAAT 1866
Db 1313 GAGTATGATCTTAAATTAATCTTAACTGGCTTCAATGACAGAGACTGAAAACAAAT 1254
QY 1867 ATTTTCAGATGCTTCCACAGGCCCCCTACCTGTGCAAAATCCTCATCTCTGA 1926
Db 1253 ATTTTCAGATGCTTCCACAGGCCCCCTACCTGTGCAAAATCCTCATCTCTGA 1194
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QY 2407 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2466
Db 713 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654
QY 2467 CTTTTTGTGATATATAATGTCAGATGCAATTTGTTGGTGGATTTCCAAAGCACTTGA 2526
Db 653 CTTTTTGTGATATATAATGTCAGATGCAATTTGTTGGTGGATTTCCAAAGCACTTGA 594
QY 2527 ATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2586
Db 593 ATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534
QY 2587 AGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2646
Db 533 AGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474
QY 2647 ATGGCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2706
Db 473 ATGGCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 414

QY	2707	TAGATATAGGATGATCTTTGCTGCTGTTTATTAATTAATTAATTAATTAATTTTAAATT	2766
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QY	2767	AACATGAACACCCCTTGAGAAAATGTGTCATATCATTTCTCCAAATGCAATTTGATACAG	2826
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QY	2827	CCCATTCACCAAAATTTATCCTGACCTTCCTGACCAAAAATGATATTTATGAATATAGAA	2886
Db	293	CCCATTCACCAAAATTTATCCTGACCTTCCTGACCAAAAATGATATTTATGAATATAGAA	234
QY	2887	AAAAATACAAATTTTACAAATTTAGATTTTATTTACATATGGAATCGTATATACGTGT	2946
Db	233	AAAAATACAAATTTTACAAATTTAGATTTTATTTACATATGGAATCGTATATACGTGT	174
QY	2947	GCTTGTATTTATTAATAATTTGCTTTTAAATTTAAATTAAGCTTGAAGCAAACTATTAACCAT	3006
Db	173	GCTTGTATTTATTAATAATTTGCTTTTAAATTTAAATTAAGCTTGAAGCAAACTATTAACCAT	114
QY	3007	TGATACATATATCTACTGTGAACAGATTTTCAATACCTCGAATGTAAAGAAGACTTACTGAT	3066
Db	113	TGATACATATATCTACTGTGAACAGATTTTCAATACCTCGAATGTAAAGAAGACTTACTGAT	54
QY	3067	TATTTTCTCATGCAACTATATGTTTAAATAGAGATATATGATAGT	3113
Db	53	TATTTTCTCATGCAACTATATGTTTAAATAGAGATATATGATAGT	7

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1      RESULT 3
2      US-08-470-091-1
3      : Sequence 1, Application US/08470091
4      : Patent No. 5912236
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Xu, Hong-Ji
9      : APPLICANT: Hu, Shi-Xue
10     : APPLICANT: Benedict, William F.
11     : TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
12     : TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
13     : NUMBER OF SEQUENCES: 3
14     :
15     : CORRESPONDENCE ADDRESS:
16     : ADDRESSEE: Pennie & Edmonds
17     : STREET: 1155 Avenue of the Americas
18     : CITY: New York
19     : STATE: New York
20     : COUNTRY: U.S.A.
21     : ZIP: 10036-2711
22     :
23     : COMPUTER READABLE FORM:
24     : MEDIUM TYPE: Floppy disk
25     : COMPUTER: IBM PC compatible
26     : OPERATING SYSTEM: PC-DOS/MS-DOS
27     : SOFTWARE: PatentIn Release #1.0, Version #1.25
28     :
29     : CURRENT APPLICATION DATA:
30     : APPLICATION NUMBER: US/08/470,091
31     : FILING DATE: JUN-16-1995
32     : CLASSIFICATION: 514
33     :
34     : PRIOR APPLICATION DATA:
35     : APPLICATION NUMBER: US/08/038,760
36     : FILING DATE:
37     :
38     : ATTORNEY/AGENT INFORMATION:
39     : NAME: Poissant, Brian M
40     : REGISTRATION NUMBER: 28,462
41     : REFERENCE/DOCKET NUMBER: 7409-025-999
42     :
43     : TELECOMMUNICATION INFORMATION:
44     : TELEPHONE: (212) 790-9090
45     : TELEFAX: (212) 869-9741/8864
46     : TELEX: 66141 PENNIE
47     :
48     : INFORMATION FOR SEQ ID NO: 1:
49     : SEQUENCE CHARACTERISTICS:
50     : LENGTH: 3232 base pairs
51     : TYPE: nucleic acid
52     : STRANDEDNESS: double
53     : TOPOLOGY: not relevant
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?      MOLECULE TYPE:  DNA
?
?      FEATURE:
?      NAME/KEY:  CDS
?      LOCATION:  19..2469
?
US-08-470-091-1

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Query Match      99.88;   Score 3105.4;   DB 2;   Length 3222;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 3106;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0
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QY	7	ATGTCAGACGCTGTGAAGAGATATGATGATGATGTCAGCTCTCAGCAAAATGGAAAG	66
Db	124	ATGTCAGACGCTGTGAAGAGATATGATGATGTCAGCTCTCAGCAAAATGGAAAG	183
QY	67	ACACTGGAACCTTATATATTTGACACACACCCAGACAGTTCGATCTCAATTAATCT	126
Db	184	ACACTGGAACCTTATATATTTGACACACACCCAGACAGTTCGATCTCAATTAATCT	243
QY	127	GCATTGGTCTTAAAGTTTCTTGATACATTTTATATAGCTAAAGGGAATATTACA	186
Db	244	GCATTGGTCTTAAAGTTTCTTGATACATTTTATATAGCTAAAGGGAATATTACA	303
QY	187	ATGGAAGATGATGTCGTGATTTTCAATTTCAAGTAAAGCTATGTCCTTGACATTTTAT	246
Db	304	ATGGAAGATGATGTCGTGATTTTCAATTTCAAGTAAAGCTATGTCCTTGACATTTTAT	363
QY	247	AAACTCTACCCCATGTTGTGCTCAAGAACCATTAAGACAGCTGTTTATACCCTTAT	306
Db	364	AAACTCTACCCCATGTTGTGCTCAAGAACCATTAAGACAGCTGTTTATACCCTTAT	423
QY	307	GGTTCACTCGACACCCAGCGAGCTCAGAACGAGTGCAGGATACCAAAACACTA	366
Db	424	GGTTCACTCGACACCCAGCGAGCTCAGAACGAGTGCAGGATACCAAAACACTA	483
QY	367	GAAATGATACAGAATTTATGGAAGTTCTCTGTAAGAAGATGAATGTATATAGTAG	426
Db	484	GAAATGATACAGAATTTATGGAAGTTCTCTGTAAGAAGATGAATGTATATAGTAG	543
QY	427	GTTAAAAATGTTTATTTTCAAAAAATTTTATACCTTTATGAATTCCTGTGACTGTACA	486
Db	544	GTTAAAAATGTTTATTTTCAAAAAATTTTATACCTTTATGAATTCCTGTGACTGTACA	603
QY	487	TCTATATGACTCCAGAGGTTGAAAACTCTTGTAAAGCATACAGAGAAATTTATCTTAA	546
Db	604	TCTATATGACTCCAGAGGTTGAAAACTCTTGTAAAGCATACAGAGAAATTTATCTTAA	663
QY	547	AATTAAGACATAGATGACAGATTTATTTTGGATCATGATTAATAACTCTGTACAGCTATCT	606
Db	664	AATTAAGACATAGATGACAGATTTATTTTGGATCATGATTAATAACTCTGTACAGCTATCT	723
QY	607	ATTGACAGTTTTGAAACACACAGACAGACACACAGAAATAAAGCTGTATGAGAGGTGAT	666
Db	724	ATTGACAGTTTTGAAACACACAGACAGACACACAGAAATAAAGCTGTATGAGAGGTGAT	783
QY	667	GTAATTTCTCCACACACTCCAGTTTASAGACTGTTATGAACACTATCCACAAATTAATGATG	726
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QY	727	ATTTTAAATTCACGACAGTATCAACCTTCAGAAAAATCTGATTTCTATTTTAAACAACGCG	786
Db	844	ATTTTAAATTCACGACAGTATCAACCTTCAGAAAAATCTGATTTCTATTTTAAACAACGCG	903
QY	787	ACAGTGAATCCAAAAGAAAGATATATGCAAAAGAGGATTTTATAGATATACATCTTTTAA	846
Db	904	ACAGTGAATCCAAAAGAAAGATATATGCAAAAGAGGATTTTATAGATATACATCTTTTAA	963
QY	847	GAAATAATTTGTAAMGCTGTGGAGACAGGCTGTCTGCCAAAATGTGATCACAGGATACAA	906
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QY	907	CTTGAGATTCGCTGTGTATACGAGTAATGAATCATGCTTTAAATCAGAGAGAACGA	966
Db	1024	CTTGAGATTCGCTGTGTATACGAGTAATGAATCATGCTTTAAATCAGAGAGAACGA	1083

Oy	967	TTTTCGATTCGAAATTTTTCAGCAACCTTCGATGAGCAACATTTTCATATAGCTTATATG	1026
Oy	967	TTTTCGATTCGAAATTTTTCAGCAACCTTCGATGAGCAACATTTTCATATAGCTTATATG	1026
Db	1084	TTATTCATTCGAAATTTTTCAGCAACCTTCGATGAGCAACATTTTCATATAGCTTATATG	1143
Oy	1027	GGGTGGGCTCTGAGGTGTGTAATGSCCAATATAGCAGAGTACATTCAGATCTTGAT	1086
Db	1144	GGGTGGGCTCTGAGGTGTGTAATGSCCAATATAGCAGAGTACATTCAGATCTTGAT	1203
Oy	1087	TCGTGACAGATTTGTCTTTCCCATGATTCGATGTGCTATATTTAAACCCCTTGAT	1146
Db	1204	TCGTGACAGATTTGTCTTTCCCATGATTCGATGTGCTATATTTAAACCCCTTGAT	1263
Oy	1147	TTTTTCAAGAGATGCAAGATTTTATTCAGAGAGCAAGCAACTGCAAGAGAAATGATA	1206
Db	1264	TTTTTCAAGAGATGCAAGATTTTATTCAGAGAGCAAGCAACTGCAAGAGAAATGATA	1323
Oy	1207	AAACATTTTGAAGCATGTGAAACATTCAGATTCAGATTCGATGAGCTTCACATTTCA	1286
Db	1324	AAACATTTTGAAGCATGTGAAACATTCAGATTCAGATTCGATGAGCTTCACATTTCA	1383
Oy	1267	CGTTTATTTGATCTTATTTAAACATCAAGAGACGAGAGCACACTGATCATCTTGAA	1326
Db	1384	CGTTTATTTGATCTTATTTAAACATCAAGAGACGAGAGCACACTGATCATCTTGAA	1443
Oy	1327	TCGTGCTGTCCCTTAAATCTTCCCTCCAGAAATATTCACATGAGACAGATATGATGTT	1386
Db	1444	TCGTGCTGTCCCTTAAATCTTCCCTCCAGAAATATTCACATGAGACAGATATGATGTT	1503
Oy	1387	TCCTCGTTAGATGCCCAAGAAAAAGTTTAACATACGCTGAAATTTCTACTGCAAT	1446
Db	1504	TCCTCGTTAGATGCCCAAGAAAAAGTTTAACATACGCTGTAATTTCTACTGCAAT	1563
Oy	1447	GCAGAGACACAGCAACCTCAGGCTCCAGACCCAGAGAAAGCATGTGAATCTACCTCT	1506
Db	1564	GCAGAGACACAGCAACCTCAGGCTCCAGACCCAGAGAAAGCATGTGAATCTACTCTCT	1623
Oy	1507	TCACTGTGTTTATAAAAAGTGATATCGGCTATGCTCGGGCTAAATATACCTTTGTA	1566
Db	1624	TCACTGTGTTTATAAAAAGTGATATCGGCTATGCTCGGGCTAAATATACCTTTGTA	1683
Oy	1567	CGGCTCTCTGTGAGCAACCCAGAAATTTAGAACATATCATCTGAGACCTTTTTCAGACAC	1626
Db	1684	CGGCTCTCTGTGTGAGCAACCCAGAAATTTAGAACATATCATCTGAGACCTTTTTCAGACAC	1743
Oy	1627	CTCGACATAGATATGAACTCATGAGAGACAGCAATTTGGACCAATATATGATGTGTC	1686
Db	1744	CTCGACATAGATATGAACTCATGAGAGACAGCAATTTGGACCAATATATGATGTGTC	1803
Oy	1687	ATGTATGCGATATGGAAGAGGAAGATATAGACCTTAAATTCMAAATCANTGTAGACACA	1746
Db	1804	ATGTATGCGATATGGAAGAGGAAGATATAGACCTTAAATTCMAAATCANTGTAGACACA	1863
Oy	1747	TACAGAGATCTTCTCATGCTGTTTCAGAGACATTTCAAGCTGTTTTGATCAAGAGAG	1806
Db	1864	TACAGAGATCTTCTCATGCTGTTTCAGAGACATTTCAAGCTGTTTTGATCAAGAGAG	1923
Oy	1807	GACTATGATTTCTATATAGTATTTCTATTACTCGATCTTCATGACGAGACTGAAAACAAT	1866
Db	1924	GACTATGATTTCTATATAGTATTTCTATTACTCGATCTTCATGACGAGACTGAAAACAAT	1983
Oy	1867	ATTTTTCATATGCTTCACAGAGCCCTTACTCTGTACCAATACCTCACAATCTCTGCA	1926
Db	1984	ATTTTTCATATGCTTCACAGAGCCCTTACTCTGTACCAATACCTCACAATCTCTGCA	2043
Oy	1927	AGCCCTTACAACTTTCTAGTTCACCCCTTACGAGATTCCTGAGAGGAACATCTATATTCA	1986
Db	2044	AGCCCTTACAACTTTCTAGTTCACCCCTTACGAGATTCCTGAGAGGAACATCTATATTCA	2103
Oy	1987	CCCTCTAAGAGTCATATAAAATTTTCAGAGGTCTGCCAACACCAACAAAAATGACTCA	2046
Db	2104	CCCTCTAAGAGTCATATAAAATTTTCAGAGGTCTGCCAACACCAACAAAAATGACTCA	2163

QY	2047	ATACAAAGAACTCTTGATATTCATATGGTGAATCATATTCGGGACTCTTGAGACTCCAGAAA	2106
DB	2164	AGATCAAGATCTTGTGTTCATATGGTGAATCATATTCGGGACTCTTGAGAACTTCCAGAAA	2223
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DB	2224	ATTAATTCAGATGGTATGTATACAGCCAGCTGTGTCCAAAGAAAGTGTGAGAAAGAACAC	2283
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DB	2284	CCCTCCTAACCCACTAAAAAATCTACGCTTTGATATTGGAAGATCAGATGAGCAGATGGA	2343
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DB	2404	CGAAACCGAATCGAAACACAAATGSAATGATAGATGATGATACCTCAAAACGAGAAAG	2463
QY	2347	AAATGAGATCTCAGAGACCTTGTTGGACACTGTGTACACTCTGATTCATTTGTCTCTCA	2406
DB	2464	AAATGAGATCTCAGAGACCTTGTTGGACACTGTGTACACTCTGATTCATTTGTCTCTCA	2523
QY	2407	CAGATGTGACTGTATTAACCTTCCAGAGTTCTGTATTATGGCACATTTAATATCTTCAGCT	2466
DB	2524	CAGATGTGACTGTATTAACCTTCCAGAGTTCTGTATTATGGCACATTTAATATCTTCAGCT	2583
QY	2467	CTTTTGTGGATATTAATAATGTGCAGATGCAATGTTGGGTGATCTCCTAAGCAGACTGGA	2526
DB	2584	CTTTTGTGGATATTAATAATGTGCAGATGCAATGTTGGGTGATCTCCTAAGCAGACTGGA	2643
QY	2527	ATGTGTGATCATTTGTAATTTATATACAAAGATGSAANAATCTGTGTAAATCCGTCGCAATTA	2586
DB	2644	ATGTGTGATCATTTGTAATTTATATACAAAGATGSAANAATCTGTGTAAATCCGTCGCAATTA	2703
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DB	2704	AGTGTATGCAGATGTGTTCTCTTCCAAAGTAATATGCTGTCTTATGAGATAGTAAAGA	2763
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DB	2764	ATGAGCCCTAGAGTGGAGTCTCTGATTAACCCAGCCGCTGTGACTACTTGCCTCTCTTG	2823
QY	2707	TAGCATATAGAGTGAATGTTGCTGTGTTTATATTAATTAATATATATATTTTAAAT	2766
DB	2824	TAGCATATAGAGTGAATGTTGCTGTGTTTATATTAATTAATATATATTTTAAAT	2883
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DB	2884	AACATGGAACCCCTTAGAANAATGTGCTATCATATGCCAAATGCAATTTGATACAG	2943
QY	2827	CCCATTCACAAATTAATCTCGAACCTTCTGCAAAATGATATTAATGAAATTAAGAA	2886
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DB	3004	AAAAATTAATAATTTACACATATGATTTATTTACTATTTGGAATCTGATTAATCTGT	3063
QY	2947	GCTGTTTTTAAATTTTGCCTTTAATTAATTAATAAGCTGGAGCAAACTATATACATA	3006
DB	3064	GCTGTTTTTAAATTTTGCCTTTAATTAATTAATAAGCTGGAGCAAACTATATACATA	3123
QY	3007	TGATATCATCATATATATATGAAACGATTTATATCCGACAAATATATTAAGAAACCTTACTGT	3066
DB	3124	TGATATCATCATATATATATGAAACGATTTATATCCGACAAATATATTAAGAAACCTTACTGT	3183
QY	3067	TATTTTCTTCATCAACTATATGTTTTTAATGAGATTAATGATAGT	3113
DB	3184	TATTTTCTTCATCAACTATATGTTTTTAATGAGATTAATGATAGT	3230

RESULT 4
US-08-470-091-2/c
Sequence 2, Application US/08470091
Patent No. 5912236
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
APPLICANT: Benedict, William F.
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
METHOD OF SEQUENCES: 3
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,091
FILING DATE: JUN-16-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US/08/038,760
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
US-08-470-091-2

Query Match 99.8%; Score 3105.4; DB 2; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 3053 ACATGGAACCTATATATTTGACACACCCAGAGTGTGATATGACGAATTAATTC 2994
QY 127 GCATTGCTGCTAAAGTCTTGATCACAATTTTATAGTAAAGGGAATATACAA 186
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DB 2933 ATGGAAGATGATCTGATTTTATGATTAATGTAATGTCCTGATATATTTAT 2874
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DB 2873 AACCTGCACTCCATCTGCTCAAGAACCATATTAACAGCTGTTATACCATTAAT 2814
QY 307 GGTTACCTGCAACCCAGGCGAGGTGCAAGACAGAGTGCAGCAAAACACTA 366
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DB 2813 GGTTACCTGCAACCCAGGCGAGGTGCAAGACAGAGTGCAGCAAAACACTA 2754
QY 367 GAAATGATACAGAAATTTATGAAGTTCTCTGTAAGAACATGATTAATATGATGAG 426
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QY 427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAATTTCTGACCTGTACA 486
DB 2693 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAATTTCTGACCTGTACA 2634
QY 487 TCTAATGACTCCAGAGTTGAAAAATCTTCTAAGCATACGAAGAATTTATCTTAAA 546
DB 2633 TCTAATGACTCCAGAGTTGAAAAATCTTCTAAGCATACGAAGAATTTATCTTAAA 2574
QY 547 AATTAAGATCTGATGCAAGATTTATTTGATGATGTAATTAACCTTCAGAGATTC 606
DB 2573 AATTAAGATCTGATGCAAGATTTATTTTGTGATGTAATTAACCTTCAGAGATTC 2514
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QY 967 TTAATCATTCAAAAATTTATGCAAACTTCGAAATGCAACATTTTCATATCTTTATG 1026
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DB 1733 TCTGCTGTAAGATCTCCAAAGAAAAAGGTCAACTAGCGGTGTAATTTCTAGTCAAT 1674

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Page 10

Db	2500	ACCCCTTCACAAAGTTCCTAGTTCACCCCTTACCGATTCCTCGAGGACACATCTATATTTC	2555
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Qy	2347	AAATGAGATCTCAGAGACTTGGGAGACACTGTGTAACCTCTGGATTCATTGTCTCTA	2406
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US-08-482-627-4			
Sequence 4, Application US/08482627			
Patent No. 598134			
GENERAL INFORMATION:			
APPLICANT: Lee, Men-Hen			
APPLICANT: Lee, Eva Y.H.P.			
TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor			
TITLE OF INVENTION: and Regulator			
NUMBER OF SEQUENCES: 5			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Campbell and Flores			
STREET: 4370 La Jolla Village Drive, Suite 700			
CITY: San Diego			
STATE: California			
COUNTRY: United States			
ZIP: 92122			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/482,627			
FILING DATE: 07-JUN-1995			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/951,947			
FILING DATE: 28-SEP-1992			
ATTORNEY/AGENT INFORMATION:			
NAME: Campbell, Cathryn A.			
REGISTRATION NUMBER: 31,815			
REFERENCE/DOCKET NUMBER: P-OC 1707			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (619) 535-9001			
TELEFAX: (619) 535-8945			
INFORMATION FOR SEQ ID NO: 4:			

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QY 1567 CGCCTTGTCTGTGAGACCCAGAAATGAAATATCACTGACCCCTTCCAGACACC 1626
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QY 1687 ATGATGAGCATATGCAAAAGTGAAGATATGACCTTAAATTCAAAATCATTTGTAACGA 1746
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Db 2380 GAGTATGATCTTATATGATTTCTATATCTCGGCTTCTTACGAGAGATGAAAACAAAT 2439
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Db 2500 AGCCCTTACAAGTTTCTTACCTTACCTTACCTTACCTTACCTTACCTTATTTTCA 2559
QY 1987 CCCCTGAAGATCATATATAAATTTTGAAGGTCTGCCAACACCAACAAAATGACTCCA 2046
Db 2560 CCCCTGAAGATCATATATAAATTTTGAAGGTCTGCCAACACCAACAAAATGACTCCA 2619
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Db 2620 AGATCAAGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2679
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RESULT 9
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Sequence 1, Application PC/TUS9410357
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: and Canji, Inc.
TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
TITLE OF INVENTION: Susceptibility Gene Product
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10357
FILING DATE: 13-SEP-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,108
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: PP-UC 1117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 139..2923
PCT-US94-10357-1

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OY	67	ACATGACACTATATATTTGACACACCCAGAGCTTCATATCTACGAGAAATTAATCT	126
DB	640	ACATGACACTATATATTTGACACACCCAGAGCTTCATATCTACGAGAAATTAATCT	699
OY	127	GCATTGGCTGTAAGTCTTCGAGACACATTTTATAGTAAAGGGAGATTTACAA	186
DB	700	GCATTGGCTGTAAGTCTTCGAGACACATTTTATAGTAAAGGGAGATTTACAA	759
OY	187	ATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	246
DB	760	ATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	819
OY	247	AAACTCTACCTCCATGTTGTCGACCAAGACCATATTAACAGCGTTTATACCATAT	306
DB	820	AAACTCTACCTCCATGTTGTCGACCAAGACCATATTAACAGCGTTTATACCATAT	879
OY	307	GGTTCACCTGACACCCAGGCGAGTCAAGACGAGTGTACCGATTCGAAACACCTA	366
DB	880	GGTTCACCTGACACCCAGGCGAGTCAAGACGAGTGTACCGATTCGAAACACCTA	939
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DB	1180	ATAGACGATTTTGAACACAGACGACACGACGACGACGACGACGACGACGACGACGAC	1239
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Db	2440	ATTTTGACATATCTTCACACAGSCCCCTTACCTGTGACACATATCTGCACATCTCTCGA	2499
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Db	2500	AGCCCTTACAGTTTCTAGTTCCACCTTCATCGCATCTCTGAGGAGACATCTATATTTCA	2559
Oy	1987	CCGCTGAAGATCCATATAAATTTCAAGAGGTCTGCAACACACACAAAATATGATCTCA	2046
Db	2560	CCGCTGAAGATCCATATAAATTTCAAGAGGTCTGCAACACACACAAAATATGATCTCA	2619
Oy	2047	AGATCAGAAATCTTATGATCAATTTGTGTGAATCATTTGGAGCTTTGAGAAATTCAGAAA	2106
Db	2620	AGATCAGAAATCTTATGATCAATTTGTGTGAATCATTTGGAGCTTTGAGAAATTCAGAAA	2679
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Page 16

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Oy	2227	ATAAATCCTCCACAGAGAGTCCAAATTTCCAGCAGAACTGGCAGAAATACCTTACT	2286
Db	2800	ATAAATCCTCCACAGAGAGTCCAAATTTCCAGCAGAACTGGCAGAAATACCTTACT	2859
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Db	2860	CGAATGAGATGCAAAAGCAGAAATGAATGATGATGATGATGATGATGATGATGATGATG	2919
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US-08-959-638-7			
Sequence 7, Application US/08959638			
Patent No. 5932210			
GENERAL INFORMATION:			
APPLICANT: Gregory, Richard J.			
APPLICANT: Willis, Ken N			
TITLE OF INVENTION: 'Daniel C.			
TITLE OF INVENTION: Methods of use			
NUMBER OF SEQUENCES: 9			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Campbell and Flores			
STREET: 4370 La Jolla Village Drive, Suite 700			
CITY: San Diego			
STATE: California			
COUNTRY: USA			
ZIP: 92122			
COMPUTER READABLE FORM:			
MEDIUM TYPE: floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/959, 638			
FILING DATE:			
CLASSIFICATION:			
PRIORITY APPLICATION DATA:			
APPLICATION NUMBER: US/08/328, 673			
FILING DATE: 25-OCT-1994			
APPLICATION NUMBER: US 08/233,777			
FILING DATE: 19-MAY-1994			
PRIORITY APPLICATION DATA:			
APPLICATION NUMBER: US 08/142,669			
FILING DATE: 25-OCT-1993			
ATTORNEY/AGENT INFORMATION:			
NAME: Campbell, Cathryn A			
REGISTRATION NUMBER: 31,815			
REFERENCE/DOCKET INFORMATION: P-CO 1192			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (619) 535-9001			
TELEFAX: (619) 535-6949			
INFORMATION FOR SEQ ID NO: 7:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 2995 base pairs			
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STRANDEDNESS: single			
TOPOLOGY: linear			
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NAME/KEY: CDS			

[illegible]

NAME/KEY: CDS
LOCATION: 139..2925
OTHER INFORMATION: /product="RB"
/note="retinoblastoma tumor suppressor"
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
us-08-328-673A-7

Query Match 77.4%; Score 2410.4; DB 4; Length 2995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 580 ATGTCAAGCTGTGAAGAAGTATGATGTTGTCATCTTCAGCAAAATGGAAAG 639
QY 67 ACATGTGAACCTATATATTTGACACACACCGAGCTTCATCTCAATTAATTC 126
DB 640 ACATGTGAACCTATATATTTGACACACACCGAGCTTCATCTCAATTAATTC 699
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DB 700 GCATTTGCTTAAGTTTCTTGATCATTTTATTTAGCTAAAGGGAGATTACA 759
QY 187 ATGAGAGATGATCTGGTGAATTCATTTCACTATGCTATGCTCCTGACTATTTAT 246
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DB 820 AAACCTCACCTCCCATGTTGCTCAAGAACCATATAAACAGCTTTATACCATTAAT 879
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DB 880 GGTTACCTCGACACCGACGAGGTGAGAACAGAGAGTGCAGATAGCAAAACACTA 939
QY 367 GAAATGATACAGAAATTTATTTGAAGTCTCTGTAAAGACATGATATATATGATG 426
DB 940 GAAATGATACAGAAATTTATTTGAAGTCTCTGTAAAGACATGATATATATGATG 999
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DB 1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAATCTCTGACTGTGA 1059
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QY 667 GTAATTCCTCCACACTCCAGTTAGAGCTGTATGAAACCTATCAACAATTAATGATG 726
DB 1240 GTAATTCCTCCACACTCCAGTTAGAGCTGTATGAAACCTATCAACAATTAATGATG 1299
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DB 1300 ATTTAAATTCAGAAAGTAACTTCAGAAAATCTGATTCCTTTTAAACAATGC 1359
QY 787 ACAGTGAATCCAAAGAAAGTATCTGAAAAAGATGAAGATATAGATACATCTTTAAA 846
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	2347	AAATGAGATCTCAGAGACCTTGTGGACACTGTACACCTCTGGATTCTATTCTCTCA	2406
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RESULT 1
US-07-708-962-1
Sequence 1, Application US/07708962
Patent No. 5262321

GENERAL INFORMATION:
APPLICANT : Livingston, David M.
APPLICANT : Ewen, Mark E.
TITLE OF INVENTION : Tumor Suppressor
NUMBER OF SEQUENCES : 1
CORRESPONDENCE ADDRESS:
ADDRESSEE : Choate, Hall & Stewart
STREET : Exchange Place, 53 State Street
CITY : Boston
STATE : Massachusetts
COUNTY : U.S.A.
ZIP : 02109

COMPUTER READABLE FORM:
MEDIUM TYPE : Floppy disk
COMPUTER : IBM PC compatible
OPERATING SYSTEM : PC-DOS/MS-DOS
SOFTWARE : Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER : US/07/708, 962
FILING DATE : 19910531
CLASSIFICATION : 435

ATTORNEY/AGENT INFORMATION:
NAME : Kennedy, Bill
REGISTRATION NUMBER : 33,407
REFERENCE /DOCKET NUMBER : DPCI 209
TELECOMMUNICATION INFORMATION:
TELEPHONE : (617) 227-5020
TELEFAX : (617) 227-7566
TELEX : 289374

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH : 2808 base pairs
TYPE : NUCLEIC ACID
STRANDEDNESS : double
TOPOLOGY : linear
MOLECULE TYPE : cDNA
HYPOTHETICAL : NO
ANTI-SENSE : NO

IS-07-708-962-1

Query Match	2.2%	Score 68.8;	DB 1;	Length 2808;
Best Local Similarity	53.1%;	Pred. No. 3.6e-07;		
Matches 170; Conservative	0;	Mismatches 147;	Indels 3;	Gaps 1;

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Dd	2000	GCTGACGCTTACGAGATCAATGTG---CTAAACTGGAATGTTTCAAATGATTCACAGAGA	2056
Oy	1601	TCACTCGAACCCTTCTACAGACACCCCTGCACAATGAGTATGAGACATGAGAGACAGC	1660
Dd	2057	AGATATGAGACGCTTTTGAAATTCACCTTATGTTCACTGCTCCGATCTATATGAAGACAGCC	2116
Oy	1661	ATTTGGACCAATATATGATGTGTTCATCATATGGAATATSCAAAGTGAAGATATATGACC	1720
Dd	2117	ATTGGAATGAGCTCCTCTCTTTGGCTCTTATATATGACCAAGATACCAAGAGAGAAA	2176
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Oy	1781	TCAAACGTGTTTTGATCAAA	1800
Dd	2237	ATTGAGAGTGTCTGCTGAAA	2256

RESULT 13
 US-08-106-493A-1
 Sequence 1, Application US/08106493A
 Patent No. 5457049
 GENERAL INFORMATION:
 APPLICANT: Antonio Giordano
 TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN P82,
 TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODINGS
 TITLE OF INVENTION: THEREFOR"
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Temple University Of The Commonwealth
 ADDRESSEE: System of Higher Education
 STREET: 406 University Services Building
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disquette, 3.50 inch, 720 KB
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/106,493A
 FILING DATE: August 12, 1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mullins, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 6056-188
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8383
 TELEFAX: (215) 568-5549
 TELEX: No. 5457049e
 INFORMATION FOR SEO ID NO.: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3249 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 23:41:58 ; Search time 250.854 Seconds

(without alignments)
7011.280 Million cell updates/sec

Title: US-09-026-459a-37

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

ched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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-DB=N_Geneseq.101002 -OPMT=fastp -SUPER=ring -MINMATCH=0.1 -LOCPCT=0
-LOOPEXT=0 -UNITS=bits -START=1 END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -TRX_SCORE=pct -TRX_MAX=100 -TRX_MIN=0 -ALIGN=15
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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24: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4017	100.0	2994	11 AA004713	Cancer suppressing
2	4017	100.0	2994	14 AA041545	Retinoblastoma gen
3	4017	100.0	2994	19 AAV40004	Retinoblastoma pro
4	4017	100.0	2994	21 AAT40287	Wild type human re
5	4017	100.0	2995	20 AAX90350	Human p110-RB reti
6	4017	100.0	2995	20 AAX00737	CDNA encoding a re
7	4017	100.0	2995	22 AAH25755	Retinoblastoma tum
8	4017	100.0	2995	22 AAD04474	Retinoblastoma tum
9	4017	100.0	2995	23 ABL50904	Retinoblastoma tum
10	4017	100.0	3113	19 AAV58445	Modified retinobla
11	4017	100.0	3218	19 AAV54991	DNA sequence of th
12	4017	100.0	3233	15 AA072690	Retinoblastoma 94k
13	4017	100.0	3266	19 AAV58444	Modified retinobla
14	4017	100.0	3266	19 AAV58445	Modified retinobla
15	4017	100.0	3323	19 AAV58446	Modified retinobla
16	4017	100.0	3392	19 AAV58442	Modified retinobla
17	4017	100.0	3455	19 AAV58441	Modified retinobla
18	4017	100.0	3461	19 AAV58447	Modified retinobla
19	4017	100.0	3554	19 AAV58452	Modified retinobla
20	4017	100.0	3555	19 AAV58440	Modified retinobla
21	4017	100.0	3555	19 AAV54990	DNA sequence of th
22	4017	100.0	4839	21 AAA29391	Human retinoblasto
23	4017	100.0	4839	21 AAZ86444	Human androgen rec
24	4017	100.0	4839	24 ABL62873	Breast cancer rela
25	4013	99.9	4597	9 AAH81369	Human retinoblasto
26	4013	99.9	2995	16 AA090059	Human retinoblasto
27	4013	99.9	4597	15 AA070536	Human retinoblasto
28	4011	99.9	4740	24 ABR66079	Human retinoblasto
29	4010	99.8	4597	20 AAX04501	Human retinoblasto
30	4002	99.6	2995	16 AA086398	Human Rb10 CDNA.
31	3902	97.2	5056	10 AAH90489	CDNA of human reti
32	3875	96.3	4579	9 AAH81261	Probe for retinobla
33	3850	95.8	3347	19 AAV58448	Modified retinobla
34	3674.5	91.5	3377	19 AAV58450	Modified retinobla
35	3667.5	91.3	3383	19 AAV58451	Modified retinobla
36	3550	88.4	3161	19 AAV58452	Modified retinobla
37	1761.5	43.9	18303	20 AAX04502	Human retinoblasto
38	1685.5	42.0	18177	10 AAH90490	DNA of human retin
39	772	19.2	3960	24 ABR83840	Human DNA sequence
40	771	19.2	4130	24 AAS94981	Nearly complete pi
41	756	18.8	2808	13 AAQ32655	Human CDNA diffe
42	729.5	18.2	4853	24 ABR84660	Human CDNA diffe
43	728.5	18.1	3249	16 AAQ82748	PRD2 retinoblastom
44	605.5	15.1	3291	23 AAS83193	DNA encoding novel
45	519.5	12.9	3210	23 ABL12861	Drosophila melanog

ALIGNMENTS

RESULT 1

AA004713 standard; CDNA; 2994 BP.

AA004713:

11-OCR-1990 (first entry)

Cancer suppressing gene (CSG).

Cancer: cancer suppressing gene; CSG; 13q14; retinoblastoma;

RB; ds.

Homo sapiens.

Location/Qualifiers
139..2922
/*tag a

XX WO9005180-A.
XX
XX 17-MAY-1990.
XX
XX 30-OCT-1989; 89WO-0004808.
XX
XX 31-OCT-1988; 88US-0265829.
XX
XX (REGC) UNIV OF CALIFORNIA.
XX
XX Lee WH, Huang HS;
XX
XX WPI: 1990-178822/23.
XX
XX P-PSDB: AAR05305.
XX
XX Controlling cancer -
XX by replacing ineffective cancer suppressing gene with cloned,
XX active gene.
XX
XX Claim 35; Page 86; 105pp; English.
XX
XX Gene is taken from human chromosome 13q14 retinoblastoma (RB) CDNA.
XX By installing a working CSG, safe and specific treatment and
XX prophylaxis can be given to cancer patients.
XX
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T; 0 other:

Alignment Scores:
Pred. No.: 0 Length: 2994
Score: 4017.00 Matches: 781
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

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DB 580 ATGTCACAGACTGTGAAGAGATGATGATGTTGTGCACTCTTACGCAAAATGGAAAG 639
QY 21 ThrCysGluLeuLeuTyrLeuThrGlnProSerSerSerLysThrGluLysAsnSer 40
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QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
DB 1900 TCTGCTTCTCTTAATCTTAACTTCTCCATCAAGATTAACATCTGACACAGATATGATCTT 1959
QY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
DB 1960 TCTCTGTAAGATCTCCAAAGAAAGTTCAACATACGCGGTATAATCTACCTCAAT 2019
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
DB 2020 GCGAGACACAAAGCAACCTCAGCTTCCACAGACGACATGAAATCTACCTCTCT 2079
QY 501 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
DB 2080 TCACGTGTTTAAATAAAGTGTATCGGCTAGCCTATCTCGGCTAATAATCACTTTGTGA 2139
QY 521 ArgLeuLeuSerGluHisAspProGluLysGluHisLleLleTrpThrLeuPheGlnHisThr 540
DB 2140 GCGCTTCTGTGACACCCGAAATTAAGAAATATATCTGACCCCTTTTCCAGACACCC 2199

Db 940 GAAATGATACAGATTAATGAGTCTGTGTAAGAACATGAAATGTAATAGATGAG 999
 QY 141 VALLYSASNVALTYRPhelysasnPhelIleProPhemeTasnSerLeuGluValThr 160
 Db 1000 GTGAAAAATGTTATTTTCAAAAAATTTTAAACCTTTATATGATTTCTTGAGACTGTGAA 1059
 QY 161 SerAsnGluLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
 Db 1060 TCTAATGAGACTTCCAGAGGTGTAATAATCTTTCTAAACGATACAGAAATTTATCTTAA 1119
 QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
 Db 1120 AATAAAGATCTAGATGCAAGATTAATTTTGGATCATGATTAACCTCTTGACACTGATTC 1179
 QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
 Db 1180 ATGAGACGTTTGAACACAGAGAACCCAGAAAAAGTAACCTTGATGAGAGGTGAAT 1239
 QY 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
 Db 1240 GTATTTCTCCACACACACTCCAGTTAGAGACTGTATGACACTATCCAAACAATTAATGATG 1299
 QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnGly 260
 Db 1300 ATTTTAATTCAGCAAGTGTATCAACCTTCAGAAAAATCTGATTTCTCAATTTTAACTGTC 1359
 QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
 Db 1360 ACAGTGAATCCAAAGAAATATCTGAAAGAGTAGAGATATAGATATCATCTTTAA 1419
 QY 281 GluLysPheAlaLysAlaValGluGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
 Db 1420 GAGAAATTTGCTAAGCTGTGGGACAGGTTGTGTAATTTGATGATCAGCATCAAA 1479
 QY 301 LeuGluValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluValArg 320
 Db 1480 CTGAGACTGTGCTGTATACCGAGTAATGAAATCCATGCTTAAATCAGAAAGAAACGA 1539
 QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
 Db 1540 TTATTCATTCAAAATTTTACCAAACTTCTGATGACAACTTTTTCATATGCTTTATATG 1599
 QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
 Db 1600 GCGTGCCCTGTGAGTTGTAATGCGCACATATGACAAAGTACATCTCGAAATCTTGAT 1659
 QY 361 SerLysThrAspLeuSerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
 Db 1660 TCTGAAACAGATTTGTCTTCCCATGGAATCTGAAATGCTTAATTTAAAAACCTTTGAT 1719
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluAsnLeuThrArgGluMetIle 400
 Db 1720 TTTTACAAGGATCGAAAGTTTATCAAGACAGAAAGCAACTTGACAAAGAAATGATA 1779
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaThrPheLeuSerAspSer 420
 Db 1780 AAACATTTAGACGATGGAACATCGAATCATGGAATCCCTTGATGCTCTCGATCA 1839
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGluProThrAspHisLeuGlu 440
 Db 1840 CCTTTATTTGATCTTATTAACAATCAAAAGACCGAGAGACCACTGATCACTTGAA 1899
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnHisThrAlaAlaAspMetTyrLeu 460
 Db 1900 TCTGCTGTCTCTTAATCTCTCTCCAGAAATATCACTGACAGCAGATATGATCTT 1959
 QY 461 SerProValArgSerProLysLysGlySerThrArgValAsnSerThrAlaAsn 480
 Db 1960 TCTCCTGTAAATCTCCAAAGAAAAAGTTCAACTAGCGGTGAATTTCTACTGCAAT 2019
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 Db 2020 GCAGAGACACAGACACTGACCTTCCAGACCCAGAAAGCAATGGAATGATCACTGCTT 2079

QY 501 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
 Db 2080 TCACGTTTATTAATAAAAGTATCGCTACCGCTATCTCCGGCTAAATATACACTTTGTGA 2139
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheLeuPheGlnHisThr 540
 Db 2140 CGCCCTTGTCTGAGCACCCAGAAATTAACAATATCATCTGGACCCCTTTTCCACACACC 2199
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
 Db 2200 CTGCAAAATGATGAACTCATGAGACAGACAGCAATTTGGACCAATTAATGATGTCTCC 2259
 QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
 Db 2260 ATGTATGCAATATGCAAGTGAAGAAATATAGACCTTAATTCAAAAATCATGATTAACAG 2319
 QY 581 TyrLysAspLeuProHisAlaValGluGlnThrPheLysArgValLeuIleLysGluGlu 600
 Db 2320 TTCAAGGATCTTCCCTCATGCTGTTCAGAGACATTTCAACCGTGTTCATCAAGAAAGAG 2379
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 Db 2380 GAGTATGATTTCTATTTATGATATCTATTAACGCTGCTTCATGACAGAGACTGAACAAT 2439
 QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 Db 2440 ATTTGAGATATGCTTCCACAGGCCCTTACCTGTGACAAATCACTCACTTCTCGA 2499
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGluGluAsnIleTyrIleSer 660
 Db 2500 ACCCTTCAAACTTCTCATGTTCCACCTTACCGATCTCTGGAGGAAACATCTTAATTTCA 2559
 QY 661 ProLeuLysSerProTyrLysIleSerGluGluLeuProThrProThrLysMetThrPro 680
 Db 2560 CCCCTGAAGAGTCCATATAAAATTTACAGAGGTCTGCCAACCAACAAATAATGACTCCA 2619
 QY 681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
 Db 2620 AGATCAAGAAATCTTGATATCAATTTGTAATCATTTGCGGACTTCTGAAAGTTCCAGAA 2679
 QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluIleSerAsn 720
 Db 2680 ATTAATACATGATGTATGACAGCCACCTGTGCTCAAAAGAAAGTCTGAAGAAAGCAAC 2739
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
 Db 2740 CCTCTAAACCACTGAAAAAATACGCTTGATTTGAAGCATGATGAAGACAGATGGA 2799
 QY 741 SerLysHisLeuProGluLysSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 Db 2800 AGTAAACATCTCCAGAGAGATCCAAATTTAGCAGAAACTGGCAGAAATGACTTCTACT 2859
 QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
 Db 2860 CGAACACGAATGCAAAAGCAGAAATGATGATAGATGATGATCAACTCAACAGAAAGAG 2919
 QY 781 Lys 781
 Db 2920 AAA 2922
 RESULT 3
 AA40004
 ID AA40004 standard; DNA; 2994 BP.
 AC AA40004;
 XX 15-FEB-1999 (first entry)
 DT Retinoblastoma protein RB.
 XX Retinoblastoma protein RB.
 DE
 XX Retinoblastoma protein RB; E2F; transcription factor; human;
 KW bladder cancer; restenosis; angioplasty; diabetic retinopathy;


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Db 1840 CCTTATTTGATCTTATTAACAATCAAGACCGAAGAGGACCACTGATCACCCTTCAA 1899
OY 441 SerAlaCysProLeuAnleuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db 1900 TCTGCTGTCTCTTAAATCTCCCTCCAGAAATATACACAGCAGAGATGTATCTT 1959
OY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db 1960 TCTCTGTAAAGATCTCAAGAAAAAGGTTCACTACGCTGATTAATCTTACGCAAT 2019
OY 481 AlaGlnThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db 2020 GCAGAGACACAAACCACTCAGCTCCAGACCCCAACCACTTGAATTAATCTACCTCTCT 2079
OY 501 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGlyGlu 520
Db 2080 TCACCTGTTTAAAAAGCTGATCGCTTACGCTTATCTCCGCTAAATACACTTTTGTCAA 2139
OY 521 ArgLeuLeuSerGlnHisProGlnLeuGlnHisLeuTyrPheThrLeuPheGlnHisThr 540
Db 2140 CGCCTTCTGTCTGACACCCAGAAATAGAACATATCATCTGACCCCTTCCAGCACACCC 2199
OY 541 LeuGlnAsnGlnTyrGlnLeuMetArgAspArgHisLeuAspGlnHisMetMetCysSer 560
Db 2200 CTGCGAATGAGATGAACTCATGAGAGACAGCATTTGGACCAATTAATGATGCTTCC 2259
OY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db 2260 ATGATGCGCATGTCAAGAAAGAAATATAGACCTTAAATTAATGATGTAACACACA 2319
OY 581 TyrLysAspLeuProHisAlaValIleGlnThrPheLysArgValLeuIleLysGlnGlu 600
Db 2320 TACAAGATGCTTCTCATGCTGTTCAAGAGACATCAACGCTTTTGATCAAGAAAGAG 2379
OY 601 GlnTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db 2380 GAGTATGATCTTATTAATGATTAATCTCACTCGCTTATCAAGACTGAAACCAAT 2439
OY 621 IleLeuGlnTyrAlaSerThrArgProThrThrLeuSerProIleProHisIleProArg 640
Db 2440 ATTTGCGAGTATGCTTCACACAGCCGCCACCTGTGCACCAATCTCACATTCCTCGA 2499
OY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlnLysAsnIleTyrIleSer 660
Db 2500 AGCCCTTCAAGATTCTCTAGTCAACCTTACGATTCCTGGAGGAAACATCTAATTTTCA 2559
OY 661 ProLeuLysSerProTyrLysIleSerGlnGlyLeuProThrProThrLysMetThrPro 680
Db 2560 CCCCTGAGAGCTCATATATAAATTTTCAAGAGCTCTCCAAACCAACAAAAATGACTCCA 2619
OY 681 ArgSerArgIleLeuValSerIleGlyLysPheGlyThrSerGlnLysPheGlnLys 700
Db 2620 AGATCAAGAAATCTTAATATCAATTTGGATTCCTTGGGACTTTCGAGAAAGTCCAGAAA 2679
OY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGlnGlySerAsn 720
Db 2680 ATAATTCAGATGTATTAACAGCAGCCGCTGCTCAAAAAGAGTCTGAGAGGAAAGCAAC 2739
OY 721 PropolLysProLeuLysLysLeuArgPheAspIleGlnGlySerAspGlnAlaAspGly 740
Db 2740 CCTCCTAAACACGCAAAACCTAAGCTTTGATATGAGATGATGAGAGCAAGATGAGA 2799
OY 741 SerLysHisLeuProGlnGlyLysPheGlnGlnLysLeuAlaGlnMetThrSerThr 760
Db 2800 AGTAAACATCTCCAGAGAGAGTCCAAATTCACAGCAAACTGGCAAAATGACTTCTACT 2859
OY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlnGlu 780
Db 2860 CGAATCGCAATGCAAAAGCAAAATGAATGATGATGATGATGATGATGATGATGATGATG 2919
OY 781 Lys 781

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Db 2920 AAA 2922
RESULT 4
AAZ40287
ID AAZ40287 standard; cDNA; 2994 BP.
AC AAZ40287;
XX 24-FEB-2000 (first entry)
DE Wild type human retinoblastoma gene.
XX RB gene; human; retinoblastoma gene; mutation detection; immunoscreening;
XX retinoblastoma diagnosis; hereditary retinoblastoma; secondary cancer;
XX osteosarcoma; fibrosarcoma; glioblastoma; breast cancer;
XX tumorigenesis suppression; ss.
OS Homo sapiens.
XX
XX US5998134-A.
XX
XX 07-DEC-1999.
XX
XX 07-JUN-1995; 95US-0482627.
XX
XX 15-OCT-1987; 87US-0108748.
XX
XX 28-SEP-1992; 92US-0951947.
XX
XX (REBC ) UNIV CALIFORNIA.
XX
XX Lee EXP, Lee W;
XX
XX MPI: 2000-052540/04.
XX
XX P-PSDB: AAY55060.
XX
XX Detecting retinoblastoma gene-cancer in mammals -
XX
XX Example 6; Fig 7; 34pp; English.
XX
XX This sequence represents the wild type human retinoblastoma gene.
XX The invention relates to a method of detecting a mutated retinoblastoma
XX (mrb) nucleic acid in mammals comprising hybridizing an isolated
XX full-length, wild-type RB (wtRB) cDNA probe to a cell sample and
XX detecting a mutated RB nucleic acid. The method is useful as a diagnostic
XX tool for diagnosing retinoblastoma. RB cDNA or genomic DNA are preferably
XX used as probes to determine the defect region of the mrb gene through
XX genomic DNA blotting analysis or using the method of restriction fragment
XX length polymorphism analysis to determine the diseased allele. Cloned RB
XX cDNA can be used to generate specific anti-RB protein (anti-ppRB10)
XX antibodies which are useful for immunoscreening of tissue biopsy. The
XX diagnostic method is particularly intended for use in screening
XX families with a history of hereditary retinoblastoma and for screening
XX their children. It may also be used in prophylactic and postnatal
XX screening and for the prediction of the development of secondary
XX cancer, such as, osteosarcoma, fibrosarcoma, glioblastoma, breast
XX cancer whether or not connected with retinoblastoma. The method is also
XX used in the suppression of tumorigenesis where the absent RB protein
XX ppRB10 will be provided through the molecular induction and gene
XX transplanting of the RB cDNA to the individual in need of ppRB10.
XX
XX Sequence 2994 BP; 974 A; 618 C; 594 G; 808 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 2994
XX Score: 4017.00 Matches: 781
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 21 Gaps: 0
XX
XX US-09-026-459a-37 (1-781) x AAZ40287 (1-2994)
OY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGlnArg 20

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QY 741 SerLysHsIstneProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 |||
 DB 2800 AGTAAACATCTCCCGAGAGAGTCCAAATTTCAGCGAAAGCGAAGAAATGACTTACT 2859
 QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
 |||
 DB 2860 CGAACACGAATGCCAAAGCAGAAATGATGATACGATGATACGATCAACAGGAAGAG 2919
 QY 781 Lys 781
 |||
 DB 2920 AAA 2922
 RESUR 5
 AAX90350
 ID AAX90350 standard; cDNA; 2995 BP.
 XX
 AC AAX90350;
 XX
 XX 27-SEP-1999 (first entry)
 DE Human p110-RB retinoblastoma tumour suppressor encoding cDNA.
 XX
 XX Human; p110-RB; retinoblastoma; tumour suppressor; gene therapy;
 KM adenoviral protein IX; recombinant adenovirus expression vector;
 KM cell cycle; p53; mitosis; cell death; apoptosis; thymidine kinase;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 139..2925
 FT /*lag- a
 FT /product= "p110-RB"
 FT /note= "retinoblastoma tumour suppressor"
 FT
 FT
 FT
 PN US5932210-A.
 XX
 PD 03-AUG-1999.
 XX
 PF 28-OCT-1997; 97US-0959638.
 XX
 PR 25-OCT-1994; 94US-0328673.
 PR 25-OCT-1993; 93US-0142669.
 PR 19-MAY-1994; 94US-0246066.
 PR 28-OCT-1997; 97US-0959638.
 XX
 PR (CANU-) CANUJ INC.
 PR
 PR Gregory RJ, Maneval DC, Willis KM;
 DR WPI: 1999-443568/37.
 DR P-PSDB: AAY24471.
 XX
 XX Recombinant adenoviral vectors useful for gene therapy of cancer,
 PT especially p53 deficient tumours
 PS
 PS Disclosure; Fig 3; 50pp; English.
 CC The present invention describes a composition comprising a recombinant
 CC adenovirus expression vector, where the vector has an insert of
 CC exogenous DNA comprising a gene encoding a foreign protein and
 CC adenovirus DNA in which all of the coding sequences of E1a, E1b, and
 CC protein IX, and part of E3 are deleted. The vectors are useful in gene
 CC therapy treatment of cancer, especially for treating p53 deficient
 CC tumours. The vector enables safer and more efficient gene therapy of
 CC cancer. The present sequence encodes human p110-RB retinoblastoma
 CC tumour suppressor which can be used as the foreign gene in the above
 CC vector.
 SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;
 Alignment Scores:

Pred. No.: 0 Length: 2995
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0
 US-09-026-459a-37 (1-781) x AAX90350 (1-2995)
 QY 1 MetSerArgLeuLeuLysValSerPheValLeuPheAlaLeuPheSerLysLeuArg 20
 DB 580 ATGTCAAGACTGTCTCAAGAACTATGATGATGTATTGTTCACACTCTTCAGCAAAATGGAAAG 639
 QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
 DB 640 ACATGTGAACCTTATATTTATTTGACAAACCCAGAGAGTTCATATCTACATGAAATTAATTC 699
 QY 41 AlaLeuValIleuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
 DB 700 GCATTGTGCTAAAGATTCTTGGATCACATTTTATAGCTAAAGGGAGATATTACAA 759
 QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
 DB 760 ATGGAAGATGATCTGTGATTTTCATTTCAGTTAATGCTATGTCTCTGACTATTTATT 819
 QY 81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
 DB 820 AACTCTCACCTCCCATGTGCTCAAGAAACATATTAACAGCTGTATACCCATTAT 879
 QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
 DB 880 GGTTCACCTCGAAGACCCAGCGAGTCAGAACAGAGATGCGAGATAGCAAAACACTA 939
 QY 121 GluAsnAspThrArgIleIleGluValLeuCysGluLysGluCysAsnIleAspGlu 140
 DB 940 GAAATGATACAGATATTTATGAACTCTCTGTAAGAACATCATGTAATATGATGATGAG 999
 QY 141 ValLysAsnValTyrPheLysAsnPhelIleProPheMetAsnSerLeuGlyLeuValThr 160
 DB 1000 GTGAAAATGTTTATTTCAAAAATTTATCTTTATGATCTCTGTGACTGTAAACA 1059
 QY 161 SerAsnGlyLeuProGluValAlaGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
 DB 1060 TCTAATGAGACTTCAGAGAGTGAATAATCTTCTTAACAGATAGCAAGAAATTTATCTTAAA 1119
 QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
 DB 1120 AATAAAGATCTAGATGCAAGATTTATTTTGATCATGATGATGATGATGATGATGAT 1179
 QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
 DB 1180 ATAGACAGTTTGAAGACAGAGAACACACAGAACACAGAAAGATGATGATGATGATGAT 1239
 QY 221 ValIleProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMet 240
 DB 1240 GTAAATCCCTCCACACACTCCAGTACGATGATGATGATGATGATGATGATGATGAT 1299
 QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAspCys 260
 DB 1300 ATTTTAAATTCAGCAAGATGATCAACCTTCAGAAATCTGATTTCTATTTTTACACTGC 1359
 QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
 DB 1360 ACAGTGAATCCAAAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGAT 1419
 QY 281 GluLysPheAlaLysAlaValAlaGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
 DB 1420 GAGAAATTTGCTAAAGCTGTGGAGACAGGTTGTGCGAAATTTGATACACAGCATACAAA 1479
 QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
 DB 1480 CTTGAGTTTCCTGTATTACCGAGATGATGATGATGATGATGATGATGATGATGATGAT 1539

QY 321 LeuSerIleGlnAsnPheSerIleuLeuAsnAspAsnIlePheHisMetSerIleu 340
 Db 1540 TTAATCATTAATAATTTAGCAAACTTCGATGACAACTTTTCATATGCTTATG 1599
 QY 341 AlaCysAlaLeuGluValIleMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
 Db 1600 GCGTGGCTCTTGAGGTGTATGCGCAATATGACAAATGATCATCTCAAGACTTGAT 1659
 QY 361 SerGlyThrAspLeuSerPheProTrpIleIleuAsnValIleuAsnLeuLysAlaPheAsp 380
 Db 1660 TCTGGAACAGATTTCTCTTCCATGGATTCGATGCTGTTAATTTAAAGCCCTTGAT 1719
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluLysAsnLeuThrArgGluMetIle 400
 Db 1720 TTTTACAAAGTATCGAAAGTTTATCAAGACGAAGGCACTGTCAGAAAGAAATGATA 1779
 QY 401 LysHisLeuGluLysArgCysGluHisArgIleMetGluSerIleuAlaThrLeuSerAspSer 420
 Db 1780 AAACATTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCAATGGCTCGAGATTCA 1839
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
 Db 1840 CTTTATTTGACTTATTAAACATCAAGACCGAAGACCAACTGATCGACTCGAATTCA 1899
 QY 441 SerHisCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetThrLeu 460
 Db 1900 TTTGCTGTGCTCTTAATCTCTCTCGAATATATCATCATGACAGCAAGATATGATCTT 1959
 QY 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
 Db 1960 TCTCCGTAGATCTCCAAAGAAAAAGTTCAACTACGCGGTAAATTCATCGCAAT 2019
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 Db 2020 GCAGACACAAAGCAACCTCAGCCCTCCAGACCAAGACCAATGAAATCTACCTCTT 2079
 QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrIleuArgLeuAsnThrIleuGlu 520
 Db 2080 TCACTGTTTATTAAGATGATGATGGCTGATCGCTACCTCGGCTAAATACATCTGTGGA 2139
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrIleuPheGlnHisThr 540
 Db 2140 CGCCTTCTGTGAGCACCCAGAAATAGAACATATCATCTCGACCTTTCCAGCACCC 2199
 QY 541 LeuGlnAsnGluTyrGluIleuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
 Db 2200 CTCGACAGATGATGATGAACTCATGAGAGACGCGCATTTGGACCAATATATGATGCTCC 2259
 QY 561 MetTyrGlyIleCysLysValIleAsnIleAspLeuLysPheLysIleIleValThrAla 580
 Db 2260 ATGTATGGCATATGCAAGTGAAGATATGACCTTAAATTCAAATTCATGTATACAGCA 2319
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
 Db 2320 TAAAGAGATCTTCATCATGCTGTTCAGAGACATTCAAAGCTGTTTGTATCAAAAGAG 2379
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 Db 2380 GAGATCATCTTATATATGATATCTATTAACCTGCTTCATGACGAGACTGAAACAAAT 2439
 QY 621 IleLeuGlnTyrAlaSerThrArgProThrIleuSerProIleProHisIleProArg 640
 Db 2440 ATTTTGCAGATGCTTCCACCGCCCTTACCTTGTCACCAATACCTACATTCCTCGA 2499
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
 Db 2500 AGCCCTTACAAAGTTCTCTGTGTCACCTTACGGAATCTCGAGAGCAATCATATTTTCA 2559
 QY 661 ProLeuLysSerProTyrLysIleSerGluLysLeuProThrProThrLysMetThrPro 680
 Db 2560 CCCCTGAAGTGCATATATAAATTTCAAGAGCTGTGCCAACACCAAAATAATGACTCCA 2619
 QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysThrIleLys 700

Db 2620 AGATCAAGATATTGTATGATCATTTGATGATCATTTGAGACTTCGAGACTTCAGAA 2679
 QY 701 IleAsnGlnMetValCysAsnSerAspArgValIleuLysArgSerAlaGluGlySerAsn 720
 Db 2680 ATTAATCAATATGATGTATGACAGGACCGTGTCTTAAAGAAAGTCTGAAAGAAACAC 2739
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluLysSerAspGluAlaAspGly 740
 Db 2740 CTTCTTAACCACTGAAAAAACTACGCTTGTATATGAAGATCATGATGAGCAGATGSA 2799
 QY 741 SerLysHisLeuProGlyLysSerLysPheGlnLysLeuAlaGluMetThrSerThr 760
 Db 2800 AGTAAACATCTCCAGGAGAGTCCAAATTCACAGAAATGCGCAAAATATACTTACT 2859
 QY 761 ArgTyrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
 Db 2860 CGAACACGATGCAAAACCAAGAAATGATGATGATGATGATGATGATGATGATGATG 2919
 QY 781 Lys 781
 Db 2920 AAA 2922
 RESULT 6
 AAX00737
 ID AAX00737 standard; CDNA: 2995 BP.
 AC AAX00737;
 XX
 DT 13-APR-1999 (first entry)
 XX
 DE cDNA encoding a retinoblastoma protein designated pRB-110 or p110-RB.
 XX
 KW Retinoblastoma protein; RB protein; pRB-110; p110-RB; inhibition;
 KW proliferation; cancer; retinoblastoma; secondary osteosarcoma;
 KW breast cancer; small-cell lung cancer; fibrosarcoma; ss.
 XX
 OS Homo sapiens.
 XX
 FH
 FT Key
 FT CDS
 FT Location/Qualifiers
 FT 139..2925
 FT /tag= a
 FT /product= RB-protein
 FT /trans_except= (pos: 226..228, aa: Glu)
 XX
 PN US851991-A.
 XX
 PD 22-DEC-1998.
 XX
 PE 13-SEP-1994; 94US-0306513.
 XX
 PR 13-SEP-1994; 94US-0306513.
 PR 31-AUG-1987; 87US-0091547.
 PR 17-SEP-1987; 87US-0098612.
 PR 15-OCT-1987; 87US-0108748.
 PR 31-OCT-1988; 88US-0265829.
 PR 11-JUL-1990; 90US-0550877.
 PR 16-JUL-1990; 90US-053892.
 PR 16-JUL-1990; 90US-0553905.
 PR 17-OCT-1991; 91US-0778510.
 PR 14-JUL-1992; 92US-0914039.
 PR 02-OCT-1992; 92US-0956472.
 PR 17-JUN-1993; 93US-0079207.
 PR 13-SEP-1993; 93US-0121108.
 PR 24-SEP-1993; 93US-0126810.
 XX
 PA (CAND-) CANTI INC.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
 PI Wang NP;
 XX
 DR WPI; 1999-080477/07.

DR P-PSDB; AAW67801.

PT Inhibition of cancer cell proliferation - with retinoblastoma protein or polypeptide

PS Example 1; Fig 2A-K; 72pp; English.

CC The present sequence encodes human retinoblastoma (RB) protein
CC designated pRB-110 or p110-RB. The protein is used in a method
CC for inhibiting proliferation of pathologically proliferating cells
CC lacking endogenous functional retinoblastoma protein. The method
CC comprises contacting the cells with a polypeptide comprising a 56 kD
CC C-terminal fragment of retinoblastoma protein. The method is useful
CC for treating cancers, especially retinoblastoma or secondary
CC osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.

SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:

NO.:	0	Length:	299
Percent:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-026-459A-37 (1-781) x AAX00737 (1-2995)

Qy	1	MSerAa	gLeuLeuLeuLysLysTrpAspValLeuPheAlaLeuPheSerLysLeuIu	20
Db	580	ARGTMA	AGCTTTGAAGAAAGATGATATTTTGGACACTTCAGCAAAATGGAAAG	639
Qy	21	ThrCys	LeuLeuLeuLeuLeuThrGlnProSerSerLLeuThrGluLeuAsnSer	40
Db	640	ACATGTGA	ACTTATATATATTTGACAAACCCAGAGTGCATATCTACTGAAATTAATCT	699
Qy	41	AlaLeuVal	LeuLeuValSerTrpLeuPheLeuLeuAlaLysGluValLeuGln	60
Db	700	GGATTGGT	GCCTAAAGCTTTCTTGATCACATTTTATAGCTAAAGGGAGATATTACAA	759
Qy	61	MetGluAsp	AspLeuValLeuSerPheGlnLeuMetLeuCysValLeuAspLysPheLe	80
Db	760	ATGGAAAC	TGATGGCTGATTTTCATTCAGTAAAGCATGTGCTGATGACATTATTTAT	819
Qy	81	LysLeuSer	ProCProMetLeuLeuLysGluProCysTrpLysTrpAlaValLeuProLeuAsn	100
Db	820	AAACCTCA	CTCCTCCATCTGGTCTCAAGAACCTATATAAAACAGCTGTATATCCCATTAAT	879
Qy	101	GlySerPro	ArgThrProArgArgGluGlnAsnArgSerAlaArgLeuAlaLysGlnLeu	120
Db	880	GGTCTACT	CGAACACCCAGCGGAGGTCACAAACAGAGTGCACGATACCCAAACAACTA	939
Qy	121	GluAsnAsp	ThrArgLeuLeuGluValLeuCysLysGluHisGluCysAsnLLeuAspGlu	140
Db	940	GAATATGAT	CAACAAATTTATGAAGTCTCTGTAAAGAACATGAATATATATATGATG	999
Qy	141	ValLysAsnVal	TrpPheLysAsnPheLeuProPheMetAsnSerLeuGluLeuValThr	160
Db	1000	GGGAAAAA	TGTTATTTTCAAAAAATTTTATACCTTTATGAATTCCTGTGACCTTTACA	1050
Qy	161	SerAsnGlyLeu	ProLuuValGluAsnLeuSerLysArgTrpGluGluLeuLeuLysTrpLeuLys	180
Db	1060	TCTAATGAC	CTTCACAGAGGTGAAAAATCTTTCAACACATACGAAGAAATTTATCTTAAA	1111
Qy	181	AsnLysAsp	LeuAspAlaTrpGluPheLeuAspHisAspLysTrpLeuGlnThrAspSer	200
Db	1120	ATAAAGAT	CTTCAATATATTTTGTGATCATGATATAAACTCTCAAGCAATATCT	117
Qy	201	LLeuAspSer	PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn	220
Db	1180	ATAGACAG	CTTTTAAACACAGCAACACCCGAAAAAGCACTCTGATGAAGAGGTGAT	1233
Qy	221	ValLLeuPro	ProHisThrProValArgThrValMetAsnThrLeuGlnLeuMetLeu	240

Db 2320 TACAAGGATCTTCGATGCTGTCAGAGACATCAACGTTTGTGTCAAAGAGAG 2379
 QY 601 GturyaspSerIleIleValIpheTyAsnSerValIphemeGlnArgLeuLysThrAsn 620
 Db 2380 GAGTATGATTCAT 2439
 QY 621 IleLeuGlnTyAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 Db 2440 ATTTTGCAGTATGCTTCACACAGGCCCTTACTTGTACACATTAACCTACATCTCTGA 2499
 QY 641 SerProTyLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyIleSer 660
 Db 2500 ACCCTTCACAGTTTCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG 2559
 QY 661 ProLeuLysSerProTyLysIleSerGlyGlyLeuProThrProThrLysMetThrPro 680
 Db 2560 CCCCTGAAGAGTCATATAAATTTGAGAGAGTCGTCGAACACCAACAAATATGACTCCA 2619
 QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGlyLysPheGlnLys 700
 Db 2620 AGATCAAGATCTTATGATCAATGATGATGATGATGATGATGATGATGATGATGATG 2679
 QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGlyLysSerAsn 720
 Db 2680 ATAAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2739
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGlyLysSerPheGlnLysPheGly 740
 Db 2740 CCTCTAAACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2799
 QY 741 SerLysHisLeuProGlyLysSerLysPheGlnGlnLysLeuAlaIleMetThrSerThr 760
 Db 2800 ACTAAACATCTCCACGAGAGACTCCAAATTCACACAACTGCGAAGAAATGACTTCTACT 2859
 QY 761 ArgThrArgMetGlnLysGlnLysMetLysAspSerMetLysPheSerAsnLysGlnGly 780
 Db 2860 CGAAGACGATGCAAAAGCAAAATATGATGATGATGATGATGATGATGATGATGATG 2919
 QY 781 Lys 781
 Db 2920 AAA 2922
 RESULT 7
 AAH25755
 ID AAH25755 standard; DNA; 2995 BP.
 XX
 AC AAH25755;
 XX 14-AUG-2001 (first entry)
 Retinoblastoma tumour suppressor gene.
 XX Retinoblastoma tumour suppressor protein; Rb; p53; cancer;
 KM adenoviral vector; gene therapy; thymidine kinase; ds.
 XX
 OS Unidentified.
 XX
 PN US2001006629-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 24-NOV-1999; 99US-0449113.
 XX
 PR 25-OCT-1994; 94US-0328673.
 PR 25-OCT-1993; 93US-0142669.
 PR 19-MAY-1994; 94US-0246006.
 XX
 PA (GREG/) GREGORY R J.
 PA (WILL/) WILLS K N.
 PA (MANE/) MANEVAL D C.
 XX
 PI Gregory RJ, Wills KN, Maneval DC;
 XX

DR WPI: 2001-397210/42.
 DR P-PSDB: AAB98945.
 XX
 PT Recombinant adenovirus expression vector comprising a partial or total
 PT deletion of a protein IX DNA and a gene encoding a foreign protein e.g.
 PT suicide protein, useful for inhibiting or reducing the proliferation of
 PT a tumour e.g. brain tumour -
 PS Disclosure: Fig 3; 39pp; English.
 XX
 CC The present invention describes an adenoviral expression vector
 CC comprising a deletion in the protein IX gene and a gene encoding a
 CC foreign protein. This vector can be used in gene therapy, particularly to
 CC introduce tumour suppressor genes into cancerous cells. Genes which may
 CC be used include p53, thymidine kinase and retinoblastoma tumour
 CC suppressor gene (Rb). The present sequence is the retinoblastoma tumour
 CC suppressor gene.
 XX
 SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other:
 Alignment Scores:
 Pred. No.: 0 Length: 2995
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-026-459a-37 (1-781) x AAH25755 (1-2995)
 QY 1 MetSerArgLeuLeuLysLysTyAspValIleuPheAlaLeuPheSerLysLeuGlnArg 20
 Db 580 AGTCGAAACAGCTGTGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 639
 QY 21 ThrGysGlnLeuIleTyLeuThrGlnProSerSerSerIleSerThrGlnLeuAsnSer 40
 Db 640 ACATGTGAACTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 699
 QY 41 AlaLeuValIleuLysValSerTrpIleThrPheLeuLeuAlaLysGlyValIleuGln 60
 Db 700 GCATTTGGTGTCTAAAGCTTCTTGATGATGATGATGATGATGATGATGATGATGATG 759
 QY 61 MetGlnAspAspLeuValIleSerPheGlnLeuMetLysCysValIleuAspTyPheIle 80
 Db 760 ATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819
 QY 81 LysLeuSerProProMetLeuLeuLysGlnProTyLysThrAlaValIleProIleAsn 100
 Db 820 AAAGCTCACCTCCCATGTTGCTCAAAAGAACATATATAAAGAGCTGTATATACCATTTAT 879
 QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
 Db 880 GGTTGACCTCGAAGACCCAGGCGAGTCAAGACAGAGAGTGCAGATGAGCAAAACAACTA 939
 QY 121 GlnAsnAspThrArgIleIleGlyValLeuLysGlyGlnIleGlnLysAsnIleAspGln 140
 Db 940 GAATATGATACAGATATATATGAAATGTTCTGTAAAGAACATGAATGATATATAGATAG 999
 QY 141 ValLysAsnValTyPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
 Db 1000 GTGAATAATGTTTATTTCAAAATTTTATACCTTTATGAAATTCCTTGAGACTGTACCA 1059
 QY 161 SerAsnGlyLeuProGlyValGlnAsnLeuSerLysArgTyGlnGlnIleTyLeuLys 180
 Db 1060 TCTAATGACCTCCAGAGCTTGAATAATCTTCTTAACGATACAGAAATTTATCTTAA 1119
 QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
 Db 1120 AATTAAGATCTAGATGCAAGATTTATTTTGTGATCATGATATAAATCTCTCAGACTGATCT 1179
 QY 201 IleAspSerPheGlnThrGlnArgThrProArgLysSerAsnLeuAspGlnIleValAsn 220
 Db 1180 ATAGACATTTTGAAGACAGAGAACACACGAAATATGATGATGATGATGATGATGATGAT 1239

OY	221	ValIleProFroHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMet	240
DB	1240	GTAATTCCTCCACACACTCAGTGTAGAGACTGTATGAACACTATCCAAATTAATGATG	1299
OY	241	IleLeuAsnSerIleSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAspCys	260
DB	1300	ATTTTAAATTCACAGACAGTGTACACCTTCAGAAATTCGATTTCTATTTTACACACTGC	1359
OY	261	ThrValAsnProLysGlnSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys	280
DB	1360	ACAGTGATCCAAAAGAAAGTACTGAAAGAAAGTGAAGGATATAGGATACATCTTTAA	1419
OY	281	GluLysPheAlaLysAlaValGlnGlnGlyCysValGluIleGlySerGlnArgTyrLys	300
DB	1420	GAGAAATTTCTTAACCTGTGGAGAGGCTGTGTCTGAAATTTGGATCCACAGCATACAA	1479
OY	301	LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg	320
DB	1480	CTTGAGTTCGCTGTGATACCGAGTAATGAAATCCATGCTTAATCAGAAAGAAACGA	1539
OY	321	LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu	340
DB	1540	TTATCCATCAAAATTTAGCAAACTTCGATGACAACTTTTCATATGCTTTATGTG	1599
OY	341	AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp	360
DB	1600	GCGTCCCTCTGTAGGTGTGAATGAGCCACATATACAGAGATACATCTCCAGAACTTGAT	1659
OY	361	SerGlyThrAspLeuSerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAsp	380
DB	1660	TCTGGAACAGATTTGTCTTCCATGATTCGAAATGTGCTTAATTTAAAGCCCTTGAT	1719
OY	381	PheTyrLysValIleGluSerPheIleLysAlaGlnGluLysLeuThrArgGluMetIle	400
DB	1720	TTTTACAAAGTGAATCCAAAGTTTATCAAGAGAGAAAGCACTTCACAGAAATGATA	1779
OY	401	LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTyrPheSerAspSer	420
DB	1780	AAACATTTACACGATGTGAACATCCAAATCAATGAAATCCCTTGATGCTTCAGATCA	1839
OY	421	ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu	440
DB	1840	CCTTATTTGATCTTATTAACATCAAGAGACCGAAGAGCACTGATCACCCTTGAA	1899
OY	441	SerIleAspProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu	460
DB	1900	TCTCTGTCTCTTAATCTCTCTCCAGAAATATCACACTGCGACGATATGATCTT	1959
OY	461	SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn	480
DB	1960	TCTCTGTAGATCTCCAAAGAAAGTTCACACTACGCGTGAATTTCTACTGCAAT	2019
OY	481	AlaIleuThrGlnAlaThrSerIlePheGlnThrGlnLysProLeuLysSerThrSerLeu	500
DB	2020	GCAAGAGACACACACCTCAGCTTCAGACCGAAGGCCATTTGAATTCACCTCTCT	2079
OY	501	SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu	520
DB	2080	TCACCTGTTTATAAAAAAGTATCGGCTAGCCTATCTCCGCGTAATAATACCTTTGGA	2139
OY	521	ArgLeuLeuSerGlnHisProGluLeuGlnHisIleIleTyrThrLeuPheGlnHisThr	540
DB	2140	CGCCTTCTGTCTGAGCACCAGAAATTAAGAAATATCATCTGAGCCCTTTCCACACACC	2199
OY	541	LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer	560
DB	2200	CTGAGAGATAGATGAACCATGAGAGACAGCATTTGGACCAATATATATGTGTTC	2259
OY	561	MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla	580
DB	2260	ATGATGCAATATGCAAAAGTAATATATGACCTTAATTCAAATCATTTGTAACGACA	2319
OY	581	TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGln	600
DB	2320	TACAGAGATCTCTCATCTCTCTCAGAGACATTCAAACCTGTTTGAATCAAGAGAG	2379
OY	601	GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn	620
DB	2380	GAGTATATCTTATATGATATCTTAACTGGCTTCATGACGAGACACTGAAACAAAT	2439
OY	621	IleLeuGlnTyrAlaSerThrArgProThrLeuSerProIleProHisIleProArg	640
DB	2440	ATTTTGCAGATCTTTCACACAGGCCCTTCACCTGTCACCAATACCTCATTTCTCA	2499
OY	641	SerProTyrLysPheProSerSerProLeuArgIleProGlyGlnAsnIleTyrIleSer	660
DB	2500	AGCCCTTACAGTTCTCTAGTTACCCCTTACCGATTCCTGGAGGAGAACATTAATTTCA	2559
OY	661	ProLeuLysSerProTyrTyrLysIleSerGluGluLeuProThrProThrLysMetThrPro	680
DB	2560	CCCTGAAAGTCCATATTAATTTCCAGAGGCTGTGCCACACACCAAAATGACTCCA	2619
OY	681	ArgSerArgIleLeuValSerIleGlyIleSerPheGlyThrSerGluLysPheGlnLys	700
DB	2620	AGATCAAGATCTTATGATCAATGCTGATCATCTCGGCACTTCTGAGAAATCCAGAAA	2679
OY	701	IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn	720
DB	2680	ATTAATCAGATGTATGTATACACGACCGCTGTGCTCAAAAGAAATGCTGAAAGACCAAC	2739
OY	721	ProProLysProLeuLysLysLeuArgPheAspIleGluLysSerAspGluAlaAspGly	740
DB	2740	CCTCTTAAACACTGTGAAAAATACGCTTGTATTTGAAGATCAGATGAAGAGATGGA	2799
OY	741	SerLysHisLeuProGlyIleSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr	760
DB	2800	AGTAACATCTCCACAGAGATCCAAATTTTCAGCAGAAATCGCAGAAATGACTTCTACT	2859
OY	761	ArgThrArgMetGlnGlnGlnMetAsnAspSerMetAspTyrSerAsnLysGluGln	780
DB	2860	CGAACACGAATGCAAAAGCAGAAATGAATGATACATGATACCTCAACAAAGAGAG	2919
OY	781	Lys 781	
DB	2920	AAA 2922	
RESULT 8			
ID	AD04474		
XX	AD04474 standard; cDNA; 2995 BP.		
XX	AD04474:		
DT	04-JUL-2001 (first entry)		
DE	Retinoblastoma tumour suppressor protein, p10RB cDNA.		
XX	Retinoblastoma; RB: tumour suppressor protein; p10RB; p53; gene therapy;		
KW	cytostatic; antithyroid; antiproliferative; adenoviral protein IX; postrals;		
KW	thyroid hyperplasia; Grave's disease; hepatocellular carcinoma; neoplasm;		
KW	benign prostatic hyperplasia; Li-Fraumeni syndrome; sickle cell anaemia;		
KW	Tay-Sachs disease; leukaemia; lymphoma; adenovirus vector; cancer; ss.		
OS	Unidentified.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	139..2925	
FT		/tag= a	
FT		/product= "Retinoblastoma tumour suppressor protein,	
FT		p10RB"	
PN	US6210939-B1.		
XX	03-APR-2001.		
XX			
XX	25-OCT-1994;	94US-0328673.	

XX 25-OCT-1993; 93US-0142669.
PR 19-MAY-1994; 94US-0233777.
XX

PA (CANU-) CANUI INC.

PI Gregory RJ, Wills KN, Maneval DC;

DR WPI: 2001-289633/30.

P-PSDB; AA00689.

XX New recombinant adenovirus expression vector having a gene encoding for
PI a foreign protein and a partial or total deletion of the adenoviral
PT protein IX DNA, useful in gene therapy for treating or reducing
PT hyperproliferative cells -

PS Disclosure; Fig 3; 4pp; English.

XX The present cDNA sequence encodes retinoblastoma (RB) tumour suppressor
CC protein, designated as p110RB.

CC The invention relates to a recombinant adenovirus expression vector
CC characterised by the partial or total deletion of the adenoviral protein
CC IX DNA beginning at nucleotides 357 or 360 and ending at 4020-4050, and
CC having a gene encoding a foreign protein such as tumour suppressor
CC protein, p110RB (retinoblastoma) and p53. Adenovirus vector is used
CC for screening tumour suppressor genes useful in gene therapy. The vector
CC is particularly useful for treating or reducing hyperproliferative cell
CC disorders such as thyroid hyperplasia, Grave's disease, psoriasis,
CC benign prostatic hypertrophy, Li-Fraumeni syndrome, cancers specifically
CC hepatocellular carcinoma, neoplasms, leukaemias, lymphomas, etc. to
CC inhibit tumour proliferation or to ameliorate particular related
CC pathology such as sickle cell anaemia and Tay-Sachs disease. The vector
CC is also useful for the safe recombinant production of diagnostic and
CC therapeutic polypeptides and proteins.

SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 2995
Score: 4017.00 Matches: 781
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-026-459A-37 (1-781) x AAD04474 (1-2995)

QY 1 MetSerArgLeuIleuLysTyrAspValIleupheAlaIleuPheSerLysLeuGluArg 20
580 ATGTCAAGACGCTGTGAAGAGATGATGATGTTGTGGACCTCTTCAGCAATTTGGAAAG 639
QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerLysSerThrGluLeuAsnSer 40
640 ACATGTGAACCTTATATTTGGACAAACCCAGAGTGCATTCACATGAAATTAATTCCT 699
QY 41 AlaIleuValIleuLysValSerTPIIleThrPheLeuLeuAlaLysGluValLeuGln 60
700 GCATTGGTGCCTAAAAGTTCTCTGGATCCACATTTTATTAAGCAAAAGGGAAGTATTCAA 759
QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
760 ATGGAAGATGATCGGTGATTTTCATTTCAATTAATGCTATGTCCTTGACATATTTATTT 819
QY 81 LysLeuSerProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
820 AAACCTCCACCTCCCATGTTGCTCAAAAGAACCATATAAACAGCTGTTATACCATTAAT 879
QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
DB 880 GGTTCACCTCGAACCCAGCCAGGTGCACACAGAGAGTGCAGGATAGCAAAACACTA 939
QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
|||||

DB 940 GAAATGATACAGAAATTTATGAAAGTTCTCTGTAAAGAACATGATTAATATAGATGAG 999
QY 141 ValLysAsnValTyrPheLysAsnPhelIleProPheMetAsnSerLeuGluValThr 160
DB 1000 GTCAAAATATGTTATTTTCAAAAATTTTATACCTTTTATGAAATTCCTTGACCTTGTAACA 1059
QY 161 SerAsnGlyLeuProGlyValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
DB 1060 TCTAAAGACCTTCAGAGGTGAAGAAATCTTCTAAACGATACGAAAGAAATTTATCTTAA 1119
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
DB 1120 AATAAAGATCTAGATGCAAGATTTATTTGGATCATGATTAACCTTCAGACGATTCCT 1179
QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
DB 1180 ATGACAGCTTTGAAACACAGACAGACACCAAGAAAGTAAACCTTGATGAAAGGTGAT 1239
QY 221 ValIleProThrIleThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
DB 1240 GTAATTCCTCCACACACTCCAGATGAGACGTGATGCAACACTATCCAAATTAATGATG 1299
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
DB 1300 ATTTTAAATTCAGCAAGATGATCAACCTTCGAAATCTGATTCCTATTTTACCAACTGC 1359
QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
DB 1360 ACAGTGAATCCAAAGAAAGATATCTGAAGAGTGAAGATATGATATCTTAA 1419
QY 281 GluLysPheAlaLysAlaValAlaGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
DB 1420 GAGAAATTTGCTAAAGCTGTGGACAGGCTTGTCTGAAATTTGGATGATACACGATACAA 1479
QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
DB 1480 CTGGAGTTCGCTGTATATACGAGTATGGAATCATCTTAATTCGAAGAAACGA 1539
QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
DB 1540 TTATCCATTTCAAAATTTTATGCAAACTTCTGAATGACAAATTTTCAATATCTTATTTG 1599
QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
DB 1600 GCGTGGCTCTTGAAGTGTGATGACCATATGACAGAAATGATCTTCAGAACTTGAT 1659
QY 361 SerGlyThrAspLeuSerPheProThrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
DB 1660 TCTGAAACGATTTGTCTTCCATGATTTCTGAATGCTTAATTTTAAAGCCTTTGAT 1719
QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluAsnLeuThrArgGluMetIle 400
DB 1720 TTTTACAAAGTGAATCGAAAGTTTATCAAAAGCAGAAAGCAACTTGACAAAGAAATATA 1779
QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTPIIleSerAspSer 420
DB 1780 AAACATTTAGAACATGATGAAACATGCAATCATGATATCCCTTGATGCTTCAGATTC 1839
QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
DB 1840 CCTTATTTGATCTTATTAACCAATCAAAAGACCGGAAAGGACCAACGATCACCTTGAA 1899
QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnHisThrAlaAlaAspMetTyrLeu 460
DB 1900 TCGGCTTGCTCTTAACTTCCTCCAGAAATTAATCACTGACAGATATGATATCTT 1959
QY 461 SerProValArgSerProLysLysGluSerThrThrArgValAsnSerThrAlaAsn 480
DB 1960 TCTCCGTGAAGTCTCCAAAGAAAGAAAGGTTCAACTACCGCTGTAAATTTCTACTGCAAT 2019
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
DB 2020 GCAGAGACACAAAGCAACTCAGCTTCAGACCCAGAACCCATGTAATCTTACTCTCTT 2079

QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
 |||||||
 Db 2080 TCACGTCTTATATAAAGTATGTCGCTACCTATCTCCGGCTAAATATACACTTGTGAA 2139
 QY 521 ArgLeuLeuSerGlnHisProGluLeuGlnHisLeileierProThrLeuPheGlnHisSer 540
 |||||||
 Db 2140 CGCCTTCTGTCTGAGCACCACCAATATACATATCATCTGACACCTTTTCCAGCACACC 2199
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
 |||||||
 Db 2200 CTCACAGATGATGATGACATGAGAGACAGCCATTGGCCAAATATGATGCTGTCC 2259
 QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysLeileValIleProAla 580
 |||||||
 Db 2260 ATGTATGGCATATGCAAAATGAGAAATATAGCTTAAATTCAAATCATATGTATACAGCA 2319
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValIleuileLysGluGlu 600
 |||||||
 Db 2320 TACAGAGATCTTCCTCATCTGTCAGAGACATTCAAACGCTGTTTGATCAAGAAAGAG 2379
 QY 601 GluTyrAspSerIleileValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 |||||||
 Db 2380 GAGATGATTCAT 2439
 QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 |||||||
 Db 2440 ATTTTGAGATGCTTCCACAGCCGCCCTTACCTGTCACCAATATCTCATCTCCGCA 2499
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
 |||||||
 Db 2500 AGCCCTTACAGATCTTCTAGTTCACCCCTTACGAGATTCCTGAGGAGCAACATATATTTCA 2559
 QY 661 ProLeuLysSerProTyrLysIleSerGluLysLeuProThrProThrLysMetThrPro 680
 |||||||
 Db 2560 CCCCTGAGAGTCCATATATAATTTTCAAGAGTGTGCCAACACCAACAAATAGACTCCA 2619
 QY 681 ArgSerArgIleLeuValSerIleLeuLysPheGlnThrSerGluLysPheGlnLys 700
 |||||||
 Db 2620 AGATCAAGAAATCTTACTATCAATATGATGATATTCGAGACTTCTGAGAGTCCAGAA 2679
 QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn 720
 |||||||
 Db 2680 ATAAATCAGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 2739
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluLysSerAspGluAlaAspGly 740
 |||||||
 Db 2740 CCTCTTAACCACTGAAAAAACTACGCTTGTATATGAGATATGATGAGATGATGATGAT 2799
 QY 741 SerLysHisLeuProGluLysSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 |||||||
 Db 2800 AGTAAACATCTCCAGAGAGTCCAAATTTTCAGCGAAACGCGCAAAATGACTTCTACT 2859
 QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluLys 780
 |||||||
 Db 2860 CGAACACGATGCAAAAGCAGAAATGATATGATATGATATGATATGATATGATATGATATG 2919
 QY 781 Lys 781
 ||||
 Db 2920 AAA 2922
 RESULT 9
 ABL50904 ID ABL50904 standard: cDNA: 2995 BP.
 XX
 AC ABL50904;
 XX
 DT 24-JUN-2002 (first entry)
 XX
 DE Retinoblastoma tumour suppressor protein p110-RB encoding cDNA.
 XX
 KW Retinoblastoma; tumour suppressor protein; p110-RB; cell cycle; p53;
 RB; mitosis; cell death; adenoviral protein IX; gene therapy; cytostatic;

KW adenovirus expression vector; tumour; non-small cell lung cancer;
 KW small cell lung cancer; hepatocarcinoma; hepatocellular carcinoma;
 KW melanoma; retinoblastoma; colorectal carcinoma; sarcoma; Wilms' tumour;
 KW astrocytoma; glioblastoma; neuroblastoma; ovarian carcinoma;
 KW osteosarcoma; renal cancer; gene; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 139..2925
 FT /tag= a
 FT /product= "retinoblastoma tumour suppressor protein"
 PN US2001016192-A1.
 PD 23-AUG-2001.
 XX
 XX 28-OCT-1997; 97US-0958570.
 XX
 XX 25-OCT-1994; 94US-0328673.
 PR 25-OCT-1993; 93US-0142669.
 PR 26-APR-1994; 94US-0233777.
 XX
 PA (GREG/) GREGORY R J.
 PA (WILL/) WILLS R N.
 PA (MANE/) MANEVAL D C.
 XX
 XX Gregory RJ, Wills KN, Maneval DC;
 DR WPI: 2001-535532/59.
 DR P-PSDB: ABB07055.
 XX
 PT New recombinant adenoviral vector comprising a partial or total
 PT deletion of a protein IX DNA and a gene encoding a foreign protein,
 PT useful in gene therapy, particularly for treating or suppressing
 PT proliferation of a tumor -
 XX
 PS Disclosure; Fig 3; 37pp; English.
 XX
 CC The present invention describes a recombinant adenovirus expression
 CC vector, which comprises a partial or total deletion of a protein IX DNA
 CC and a gene encoding a foreign protein. The recombinant adenovirus vector
 CC can have cytostatic activity and be used in gene therapy. The recombinant
 CC adenovirus expression vector is particularly useful for treating or
 CC suppressing proliferation of a tumour, e.g. non-small cell lung cancer,
 CC small cell lung cancer, hepatocarcinoma or hepatocellular carcinoma,
 CC melanoma, retinoblastoma, breast tumour, colorectal carcinoma, sarcoma,
 CC prostate tumour, bladder tumour, tumour of the reticuloendothelial
 CC tissues, Wilms' tumour, astrocytoma, glioblastoma, neuroblastoma,
 CC ovarian carcinoma, osteosarcoma or renal cancer. The present sequence
 CC encodes the retinoblastoma tumour suppressor protein p110-RB, which is
 CC given in the exemplification of the present invention.
 XX
 SO Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 2995
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 23 Gaps: 0
 US-09-026-459a-37 (1-781) x ABL50904 (1-2995)
 QY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
 |||||||
 Db 580 ATGTCAAGAGCTGTGAGAGATGATATGATATGATATGATATGATATGATATGATATGATATG 639
 QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerIleSerThrGluLeuAsnSer 40
 |||||||
 Db 640 ACATGTGACATATATATATTTGACACACCCAGCTTCGATATCTACTGATAAATATCT 699

QY	41	AlaLeuValLeuLysValSerTrpLleThrPheLeuLeuAlaLysGlyValLeuGln	60
Db	700	GCATGGTGCTAAAGATTCTTGGAACACATTTTATTAGCTAAAGGGAGCATTTACA	759
QY	61	MetGlnAspAspLeuValLleSerPheGlnLeuMetLeuGlyValLeuAspIyrPheLle	80
Db	760	ATGGAAGATGATCGTGATGATTCATTTCAGTTAAAGCATGTGCTGCATATTTAT	819
QY	81	LysLeuSerProProMetLeuLeuLysGluProIyrLysThrAlaValLleProLleAsn	100
Db	820	AAACTCTACCTCCACATGGTGTCCAAAGAACCTTTAAACAGCTGTATACCCATATAT	879
QY	101	GlySerProArgThrProArgArgLysGlnAsnArgSerAlaArgLleAlaLysGlnLeu	120
Db	880	GGTTCACCTCCGAACACCAGGCGAGGTCAAGACAGATGTCAGGATGACAAACACTA	939
QY	121	GlnAsnAspThrArgLleLleGluValLeuGlyLysGluHisGlyLysAsnLleAspL	140
Db	940	GAATAAGATACAAAGATATTTGAAGTTCCTGTAAAGACATGAATATATATATAGTAG	999
QY	141	ValLysAsnValIyrPheLysAsnPheLleProPheMetAsnSerLeuGlyLeuValThr	160
Db	1000	GTGAAAAAGTTTATTTCAAAAATTTTATACCTTTATGATTCCTCTGGACCTTGACA	1059
QY	161	SerAsnGlyLeuProGluValGlnAsnLeuSerLysArgIyrGluGluLleIyrLeuLys	180
Db	1060	TCTATAGGACTCCAGAGGTGTGAATCTTTTAAACATACGAAAGAAATTTTCTTAA	1119
QY	181	AsnLysAspLeuAspAlaArgLeuPheLeuAsnAspLysThrLeuGlnThrAspSer	200
Db	1120	AATTAAGATCTGATGCAGTCAAGCTTATTTTGGATCATGATTAACCTCTCCAGACTACT	1179
QY	201	LleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn	220
Db	1180	ATGACACGTTTGAACACACAGACACACACACAAATAACCTTGATGTAAGAGGTGAT	1239
QY	221	ValLleProProHisThrProValArgThrValMetAsnThrLleGlnLeuMetMet	240
Db	1240	GTATATTCCCTCACACACTCCAGATTAGACTGTATGAACACTATCCACAAATTAATGAT	1299
QY	241	LleLeuAsnSerAlaSerAspGlnProSerGluAsnLleLleSerIyrPheAsnGly	260
Db	1300	ATTTTAATTCAGCAAGATGATCAACCTTGAGAAATCTGATTCCTATTTTAAACAACGC	1359
QY	261	ThrValAsnProLysGluSerLleLeuLysArgValLysAspLleGlyIyrLlePheLys	280
Db	1360	ACAGTAAATCCAAAAAGAAAGATATTCGAAAAAGGAAAGATATATAGATTCATCTTTAA	1419
QY	281	GlnLysPheAlaLysAlaValGlyGlnGlyLysValGluLleGlySerGlnArgIyrLys	300
Db	1420	GAGAAATTTGCTTAAGCTGTGGGACAGGGGTGTGTCGAATTTGATTCACAGGATCAAA	1479
QY	301	LeuGlyValArgLeuIyrIyrArgValMetGlnSerMetLeuLysSerGluGluGluArg	320
Db	1480	CTTGAGGCTTCGCTGTATTTACCCAGATATAGGAATCCATGCTTAATACAGAAAGACGA	1539
QY	321	LeuSerLleGlnAsnPheSerLysLeuLeuAsnAspAsnLlePheHisMetSerLeuLeu	340
Db	1540	TTATTCATTCAAAATTTTAGCAAACTTCGATGATGACACATTTTTCATATGCTTATATG	1599
QY	341	AlaCysAlaLeuGluValValMetAlaThrIyrSerArgSerThrSerGlnAsnLeuAsp	360
Db	1600	GCGGAGGCTCTTGAGGTGTATATGGCCACATATACCAAAATGATATCTCGAATCTTGAT	1659
QY	361	SerGlyThrAspLeuSerPheProTrpLleLeuAsnValLeuAsnLeuLysAlaPheAsp	380
Db	1660	TCGGAACAGATTTGCTTTCCCTCGATGATTCGATGCTTAAATTTAAAGCCTTGAT	1719
QY	381	PheIyrLysValLleGluSerPheLleLysAlaGluGlyAsnLeuThrArgGluMetLle	400
Db	1720	TTTTACAAAGTATGAAAGATTTTATTCAAAGACAGAGGCACTTGACAAAGAAATGATA	1779
QY	401	LysHisLeuGluArgCysGluHisArgLleMetGlnSerLeuAlaTrpLeuSerAspSer	420

Db	1780	AAACATTTGGAAACGATGGAAACATCGAATCATGGAATCCCTTGATGGCTTCAGATTCA	1839
Qy	421	ProLeuPheAspLeuIleValGlnSerIysAspArgGluGlyProIleAspHisLeuGlu	440
Db	1840	CCATTATTTGATCTTATTTAAACATTCAAAGACCGGAAAGGCCAACGTATCACTTGA	1899
Qy	441	SerIleAsCysProLeuAsnLeuProLeuGlnAsnAsnHisThrIleAlaAspMetIlyLeu	460
Db	1900	TCTGCTGTGCTCCCTTAACCTTCCTCCAAATATATCACTGCAAGCATATATGATCTT	1959
Qy	461	SerProValArgSerProIlyAsValysGlySerThrThrArgValAsnSerThrIleAsn	480
Db	1960	TCTCTGTTAAAGATTCGCCAAAAAAGAGTTCACAGCGCTGTAATTTCTACTGCAAT	2019
Qy	481	AlaGluThrGlnAlaThrSerIlePheGlnThrGlnIlyProIlyLysSerThrSerIleu	500
Db	2020	GCAAGACACAAAGCAACCTCAAGCTTCACAGCCCAAGCCAACTGTAATCTACTCTCT	2079
Qy	501	SerLeuPheThrIlyLysValIlyThrArgLeuAlaIlyrLeuArgLeuAsnThrIleuCysGlu	520
Db	2080	TCACTGTTTATAAAAAGATGATCGGCTGAGCTTCCGGCTAAATTAACCTTTGAA	2139
Qy	521	ArgLeuLeuSerGlnHisProGlnLeuGlnHisIleIleThrPheIlyPheGlnHisThr	540
Db	2140	CGCTTCCTGTCTGAGACCCCAAGATTTGAACATATCATGTGGACCTTTTCCAGCACAC	2199
Qy	541	LeuGlnAsnGluIlyrGluLeuMetArgAspArgHisIleuAspGlnIleMetMetCysSer	560
Db	2200	CTCGAGATACAGATACAACTCATGAGACAGCAGCATTTGGACCAAAATTATGATGTCTCC	2259
Qy	561	MetIlyrGlyIleCysIlyValIlyAsnIleAspLeuIlyPheIlyIleIleValThrIle	580
Db	2260	ATGATGGCATATGCAAGATGAAGATATATGACCTTAAATTCAAATCATTTGTAACGCA	2319
Qy	581	TyrlIysAspLeuProHisAlaValGlnGluThrPheIlyArgValLeuIleIysGluIlu	600
Db	2320	TACAGAGATCTTCACATGCTGTCCAGAGAACATTCAAAAGCTTTTGATCAAAAGAGAG	2379
Qy	601	GluIlyAspSerIleIleValPheIlyAsnSerValPheMetGlnArgLeuIlyStrAsn	620
Db	2380	GAGATGATTCCTATATATGATGATCTTAACTCGCTTCATGACAGACATGAAACAAAT	2439
Qy	621	IleLeuGlnIlyAlaSerThrArgProThrIleuSerProIleProHisIleProArg	640
Db	2440	ATTTTGGATGATGCTCCACAGGCCCTTCACCTTCCACAAATCTCCATCTCTGCA	2499
Qy	641	SerProIlyrIlyPheProSerSerProLeuArgIleProGlyIlyAsnIleTyrlIleSer	660
Db	2500	AGCCCTTACAGATTCCTATGATTCACCCCTTACGGATTCCTGGAGGGAACATCTATTTTCA	2559
Qy	661	ProLeuIlySerProIlyIlyIleSerGluGlyLeuProThrProThrIlyMetThrPro	680
Db	2560	CCCCGACAGCTCCATATPAAATTTCCAGAAAGCTCCCAACCAACCAAAAAATGACTCCA	2619
Qy	681	ArgSerArgIleLeuValSerIleGlyIlyLysPheGlyThrSerGluIlyPheGlnIly	700
Db	2620	AGATCAAGATCTATGATTCATATGATGATTCATCTCGGACTTCGAAAGTTCCAGAAA	2679
Qy	701	IleAsnGlnMetValCysAsnSerAspArgValIleIlyIlyArgSerAlaGluIlySerAsn	720
Db	2680	ATAATTCATGATGATATGTAACAGCGACCGCTCTCAAAAGCAAGCTCGAAGGACCAAC	2739
Qy	721	ProProIlyProLeuIlyAlaIlyLeuArgPheAspIleGluIlySerAspGluIleAspGly	740
Db	2740	CCCTCTTAACACATGAAAAAACTACCGCTTGATATGTAAGAGCATCAGATGAACAGATGGA	2799
Qy	741	SerIlyHisIleuProGlyIlyLysIlyPheGlnGlnIlyIleAlaGluMetThrSerThr	760
Db	2800	AGTAAACATCTCCAGAGAGTCCAAATTTCCACAGAAACTGCGAANAATGACTCTACT	2859
Qy	761	ArgThrArgMetGlnIysGlnIlyMetAsnAspSerMetAspThrSerAsnIlyGluIlu	780

Db 2860 CGAACGATGCAAGCAAGCAAAATGATGTAGCATGATGATCTCAACAGAGAGAG 2919

Oy 781 Lys 781

Db 2920 AAA 2922

RESULT 10

AAV58445

ID AAV58445 standard; DNA; 3113 BP.

AC AAV58445;

XX 02-DEC-1998 (first entry)

XX Modified retinoblastoma tumour suppressor gene.

XX Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

XX Homo sapiens.

Key Location/Qualifiers

FT CDS 7..2352

FT /tag= a

MO9837091-AZ.

XX 27-AUG-1998.

XX 19-FEB-1998; 98MO-US03041.

XX 20-FEB-1997; 97US-0038118.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Benedict WF, Hu S, Xu H, Zhou Y;

XX WPI; 1998-480788/41.

XX P-PSDB; AAM69369.

XX Retinoblastoma suppressor protein with N-terminal modification -

XX Inhibiting cellular proliferation, particularly cancer

XX Claim 22; Page 173-177; 249pp; English.

XX This sequence encodes a modified retinoblastoma tumour suppressor

XX protein (RTSP) of the invention. The proteins can be used for inhibiting

XX cellular proliferation, when coadministered with a p53 protein. The RTSPs

XX can be used for treating diseases characterised by abnormal cellular

XX proliferation, particularly cancers. The RTSPs have a broader spectrum of

XX activity than wild type RTSPs.

XX Sequence 3113 BP; 1039 A; 577 C; 547 G; 950 T; 0 other;

US-09-026-459a-37 (1-781) x AAV58445 (1-3113)

Oy 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20

Db 7 ATGTCAAGACGTGTGAAGAGATGATGATGTTGTTCACCTCTTCAGCAAAATTTGAAAG 66

Oy 21 ThrGlySerLeuLeuLysLysTyrLeuThrGlnProSerSerSerLysSerThrGluIleAsnSer 40

Db 67 ACATGTAACTTATATATTGACACCAACGACGAGTTCGATATCTACTGAAATTAATTTCT 126

Alignment Scores:

Pred. No.: 0 Length: 3113

Score: 4017.00 Matches: 781

Percent Similarity: 100.00% Conservativeness: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 19 Gaps: 0

Oy 41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGluValLeuGln 60

Db 127 GCATTGGTGTCTAAAGAGTTCTTGTGATCACAATTTATATGCTAAAGGAGATTTACAA 186

Oy 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80

Db 187 ATGGAGATGATCTGTGTGATTTCAATTTATGCTATATGCTGATGATTTATTTATTT 246

Oy 81 LysLeuSerProPheMetLeuLeuLysGluProLysLysThrAlaValIleProIleAsn 100

Db 247 AAACCTCACCTCCACGATGCTCTCAAGAAACCATATATAACGCTTATACCCATTAT 306

Oy 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120

Db 307 GGTTACACCTCGAACACCCAGCGAGGTGCAAGACGAGTGCAGGATGCAAAACACTA 366

Oy 121 GluAsnAspThrArgIleIleGluValIleCysLysGluIleGlyCysAspIleAspGlu 140

Db 367 GAAATATGATACAAATATTTGAAGTTCTCTGTAAAGAACATGATATATATGATGAG 426

Oy 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160

Db 427 GTGAAAAATGTTTATTTTCAAAAAATTTTATACCTTTATGAAATTCCTTGACCTGTACA 486

Oy 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluIleTyrLeuLys 180

Db 487 TCTATATGAGCTCCAGAGGTTGAAGATCTTCTAAACGATACGAAAGAAATTTATCTTAA 546

Oy 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspLysAspLysThrLeuGlnThrAspSer 200

Db 547 AATAAAGATCTGATGATGCAAGATATTTTGGATCAGATTAATAACTCTTCAGCTGATCT 606

Oy 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220

Db 607 ATAGACAGTTTGAACACAGACAGACACCGAAAGATTAACCTTGATGAGAGAGTGCAT 666

Oy 221 ValIleProProIleThrProValArgThrValMetAsnThrIleGlnLeuMetIle 240

Db 667 GTAATTCCTCCACACTCCAGTATGAGACTGTATGATCACTATCCAACTATTAATGATG 726

Oy 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsn 260

Db 727 ATTTTAATTCAGCAAGATGATCAACCTTCGAAATCTGATTTCTATTTTAACTATGC 786

Oy 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280

Db 787 ACAGTGAATCCAAAGAGAGATGATGAAAGAGTGAAGATATAGCATACATCTTTTAA 846

Oy 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300

Db 847 CAGAAATTTGCTAAAGCTGTGGGACAGGGTGTGCGAAATTTGATCACAGCATACAA 906

Oy 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320

Db 907 CTTGGAGTTCCTGTTATTTACCGAGTATGAGATTCATGCTTAAATCAGAACAGACGA 966

Oy 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340

Db 967 TTATCCATTTCAAAATTTTACCAAACTTCTGAATGACAACTTTTCAATATGCTTATTT 1026

Oy 341 AlaCysAlaLeuGluValIleMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360

Db 1027 CGGTCCGCTTGTGAGGTTGTGATAGCCACATATAGCAGAAATGATCATCAGATTTGAT 1086

Oy 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380

Db 1087 TCTGCAACAGATTTGTCTTCCATGATCTGTAAGTCTTAATTTAAACCCCTTTGAT 1146

Oy 381 PheTyrLysValIleGluSerPheIleLysAlaGlyAsnLeuThrArgGluMetIle 400

Db 1147 TTTTCAAAAGATGACGAAGTTTATATCAAGCAAGGCACTTGACAAAGAAATGATA 1206

Oy 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420

QY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
112 ATGTCAGAACTGGTGAAGAAGTATGATGTTCTTCACTTCAGCAAAATGGAAAGG 171
QY 21 ThrCysGluLeuIleTyrLeuPheGlnProSerSerLysSerThrGluLeuAsnSer 40
172 ACATGTGAACCTATATATTGGACACACCCAGGTCGATTCGATCTCAATAATTCCT 231
QY 41 AlaLeuValLeuLysValSerThrPheThrPheLeuAlaLysGluValLeuGln 60
232 GCATTGGGCTAAAGATTCCTGGATCCATTTTATAGCTAAAGGAGATATACAA 291
QY 61 MetGluAspLeuValIleSerPheGlnLeuMetLeuGluValLeuAspThrPheIle 80
292 ATGGAGATGATCGTGGATTCATTCAGTTAATGCTAATGCTGCTTCACTATTTAT 351
QY 81 LysLeuSerProPheMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
352 AAACCTCACCCTCCATGCTGCTCAAGAACCATATAAAACAGCTGTATACCCATTAAT 411
QY 101 GlySerProArgThrProArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
412 GGTTCACCTCGAACCACCCAGCGAGTCCAGAAAGAGTCCAGAGATACCAAAACACTA 471
QY 121 GluAsnAspThrArgIleIleGluValLeuGluCysGluAsnIleAspGlu 140
472 GAAATATGATACAGAAATTTATGAAGTCTCTGTATAGAACATGATATATATGATGAG 531
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluValThr 160
532 GTGAAAAATGTTATTTTCAAAAAATTTTATACCTTTTATGAATCTCTGTGAGCTTATGA 591
QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
592 TCTAATGACATTCAGAGGTTGAAAAATCTTTCAACCATACAGAAATAATTTATCTTAAA 651
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
652 AATTAAGATCTAGATGCAAGATATTTTGGATCATGTATTAACCTCTCGAGCTGATTCCT 711
QY 201 IleAspSerPheGluIlePheGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
712 ATAGCAAGTTTGAACACAGAGAACACCCGAAATTAACCTTCATGACAGAGGTGAT 771
QY 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMet 240
772 GTAAATTCCTCCACACACTCCAGTTAGAGCTGTATGAACACTATCCACAAATTAATGATG 831
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnGly 260
832 ATTTTAAATTCAGCAAGTATCAACCTTCAGAAATCTGATTCCTATTTTAAACAATGC 891
QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
892 ACAGTGATCCAAAGAAAGTATACGAAAGAGTGAAGATAGATATAGATCATCTTTAAA 951
QY 281 GlyLysPheAlaLysAlaValGlyGlnGlyCysValIleGlySerGlnArgTyrLys 300
952 GAGAAATTTGCTAAAGCTGTGGACAGGCTTGTCTGCAAAATGTGATCCAGCAGATACAA 1011
QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
1012 CTTGAGAGTTCCTGTATATACGAGTAAAGATCATGCTTAAATATAGAGAGAGACGA 1071
QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
1072 TTATTCATTCATCAAAATTTTACCAAACTTCGATGATGCAACATTTTTCATATAGCTTTATATG 1131
QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
1132 CGCTCGCTCTTGAAGTGTATATGCCACATATACAGAAATACATCTCAGATCTGTAT 1191
QY 361 SerGlyThrAspLeuSerPheProThrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
1192 TCTGAGACAGATTTGTTCTTCCATGATTCGATGATGGCTATATATTTAAACCTTATAT 1251
QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluAsnLeuThrArgGluMetIle 400
1252 TTTTCAAAAGTATGCAAGATTTTATCAAGACAGAAAGCAACTTGACAGAAATGATA 1311
QY 401 LysHisLeuGluArgCysGluLysArgIleMetGluSerLeuAlaThrPheSerAspSer 420
1312 AAACATTTGAAACATGTGAACATCAATCATGATGATTCCTCTGAGGCTCCACATTTCA 1371
QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGluProThrAspHisLeuGlu 440
1372 CCTTATTTGATCTTATTAACATCAAAAGGACGAGAAAGGACCAACTGATCACTGTAA 1431
QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
1432 TCTGCTGTGCTCTTAATCTTCCCTCCAGAAATTAATCACTGCAGCAGATATGATCTT 1491
QY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
1492 TCTCCTGTAAAGTCTCCAAAGAAAAAGGTCACTACGCTGAATTTCTACTGCAAAAT 1551
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
1552 GCAGAGACCAAGACACTCAGCTTCCAGACCCAGAAAGCATTTGAATTCACCTCTCT 1611
QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGlu 520
1612 TCACGTGTTTAAAAAAAGTATCGGCTAGCGCTAGCGCTCAAAATACCTTGTGAA 1671
QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrThrLeuPheGlnHisThr 540
1672 CGGCTTCTGTGAGCACCCAGAAATTAAGAAATATCACTGAGACCTTTCACAGACACC 1731
QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
1732 CTCAGAAATGAGTATGAATCATGAGAGACAGCATTTGGACCAATATGATGATGTTCC 1791
QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValAlaThrAla 580
1792 ATGTATGGATATCCAAAGTGAAGATATAGACCTTAATTCAAAAATCATGTGAACACA 1851
QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGlu 600
1852 TACAGAGATCTTCTCATGCTGCTCAGAGACATTCAAACGTTTGTATCAAGAGAGAG 1911
QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
1912 GAGTATGATTTATATATATATATCTATTAACCTGAGCTTCATGACGAGACAGAAACAAAT 1971
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
1972 ATTTTCACATATGCTTCCACAGGCCCCCTACCTGTACCAAAATCCATCATCTCGCA 2031
QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
2032 AGCCCTTAAGATTTCCAGATTCACCTTACGGAATCTGTGAGGAGAACATCATATTTCA 2091
QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
2092 CCCCATAAGATCCATTAATTAATTCAGAGGCTCTGCCAACACCAAAATAGACTCCA 2151
QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
2152 AGATCAAGAAATCTAGATATCAATATGATGATATTCGGGACCTTGTGGAAGTTCACGAAA 2211
QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn 720
2212 ATTAATCAATATGATATGAACAGCAGCCTGTGCTCAAAAATATGCTGAAAGAGAGAAC 2271
QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740


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QY 361 SerGlyThrAspLeuSerPheProTPIleuAsnValLeuAsnLeuValAlaPheAsp 380
    |||
DB 1204 TCTGGACAGATTTGCTTCCATCGATGATTTGAAATGTCCTTAATTTAAAGCCTTGAT 1263
QY 381 PheTyrTrpValIleuGluSerPheIleuValAsnGluValAsnLeuThrArgGluMetIle 400
    |||
DB 1264 TTTTACAAAGGATGCAAAAGTTTATACAGACAGAGGACCTTGACAGAAAGAAATATA 1323
QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpPLeuSerAspSer 420
    |||
DB 1324 AAACATTTAGACAGATGTCAGATCATGGAATCCCTTGACCTGAGCTTCAGATTCA 1383
QY 421 ProLeuPheAspLeuIleuGluSerLysAspArgGluGlyProThrAspHisLeuGlu 440
    |||
DB 1384 CCTTATTATCTTATTAAACATCAAGAGCCAGAGAGGACCAACAGATGACCTTGAA 1443
QY 441 SerAlaCysProLeuAsnLeuProLeuGluAsnAsnHisThrAlaAlaAspMetTyrLeu 460
    |||
DB 1444 TCTGCTTGTCTCTTAATCTCTCTCCAGAAATATACACATGCGACGAGATATGATCTT 1503
QY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
    |||
DB 1504 TCTCTGTGAAGATCTCCAAAGAAAAAGTTCACTACGCGGTAAATTTACTGCAAT 1563
QY 481 AlaGluThrGlnAlaThrSerAlaPheGluThrGluLysProLeuLysSerThrSerLeu 500
    |||
DB 1564 GCACAGACACAGCAACCTGAGCTTCCAGACCCAGAGCCATTGAAATCTACCTCTCT 1623
QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
    |||
DB 1624 TCACGTGTTTATATAAAAGTATCGGTAGCCTATCTCCGCTAAATACACTTTGTCAA 1683
QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTPrThrLeuPheGluHisThr 540
    |||
DB 1684 CGCCTTCTGCTGACGACCCAGATTAAGAAATATCATCTGACCCCTTTCCACACACC 1743
QY 541 LeuGluAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
    |||
DB 1744 CTGCGAGATGAGTATGAACTCATGAGACAGACATTGGACAAATTTATATGTTCC 1803
QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
    |||
DB 1804 ATGATGGAATATGCAAAAGGAAATATAGACCTTAATCAATCATTTGTAACGACA 1863
QY 581 TyrTrpAspLeuProHisAlaValGluThrPheLysArgValLeuIleLysGluGlu 600
    |||
DB 1864 TACAAAGATCTCTCTGCTGTCAGAGAACATTCAAACGTTTGTATCAAGAAAGAG 1923
QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
    |||
DB 1924 GAGTATGATTCATATTATAGTATCTATTAACCTGCTTCATGCAAGACTGAAAAACAAT 1983
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
    |||
DB 1984 ATTTTGCAGTATGCTTCACACAGCCCTCTACTCTGTACCAATACCTCAATCTCCGA 2043
QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysIleTyrIleSer 660
    |||
DB 2044 AGCCCTTACAGATTCTCTAGTTCACCTTACGAGATTCTCGAGGAGAACATCTATATTTC 2103
QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
    |||
DB 2104 CCCCTGAAGAGTCCATTAATAATTTTCAGAAAGTCTGCCAACCAACAAAAATGACGCCA 2163
QY 681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGluLys 700
    |||
DB 2164 AGATCAAGAAATCTTATGATCAATTTGGTGAATCATTCGGGACTTTCGAAAGTCCAGAAA 2223
QY 701 IleAsnGluMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
    |||
DB 2224 ATAATATGATGATGTATACACGACCGTGTGCTCAAAAGAAAGTGTGAAGGAACAC 2283
QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740

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DB 2284 CCTCTTAAACACCTGAAAAAAGCTTGTGATATGAGATGAGATGAGATGGA 2343
QY 741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
    |||
DB 2344 AGTAAACATCTCCACAGAGAGATCCAAATTTTCAGCAGAAACCTGCGAGAAAGACTTACT 2403
QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
    |||
DB 2404 CGAAACACGAAATGCAAAAGCAAGAAATGAATGATACATGATACCTCAACACAGGAAG 2463
QY 781 Lys 781
    |||
DB 2464 AAA 2466

RESULT 13
AAV58444
ID AAV58444 standard; DNA; 3266 BP.
XX
AC AAV58444;
XX
DT 02-DEC-1998 (first entry)
XX
DE Modified retinoblastoma tumour suppressor gene.
XX
KM Modified retinoblastoma tumour suppressor; R1SP protein; cancer therapy;
XX cellular proliferation inhibitor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2505
FT /tag= a
PV M09B37091-A2.
XX
PD 27-AUG-1998.
XX
PF 19-FEB-1998; 98MO-US03041.
XX
PR 20-FEB-1997; 97US-0038118.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Benedict WF, Hu S, Xu H, Zhou Y;
XX WPI; 1998-480788/41.
XX DR P-PSDB; AAM69368.
XX
PT Retinoblastoma suppressor protein with N-terminal modification -
PI Inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 166-170; 249pp; English.
XX
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (R1SP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The R1SPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The R1SPs have a broader spectrum of
CC activity than wild type R1SPs.
XX
SQ Sequence 3266 BP; 1092 A; 602 C; 574 G; 998 T; 0 other;

Alignment Scores:
Pred. NO: 0 Length: 3266
Score: 4017.00 Matches: 781
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-026-459a-37 (1-781) x AAV58444 (1-3266)

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QY 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
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 Db 1297 TCGGAAACGATTTGTTTCCCATGGATTCGATGCTTAATTTAAAGCCCTTGAT 1356
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
 |||||
 Db 1357 TTTTACAAAGTATCGAAAGTTTATATCAAGACAGAGCACTTGACAGAAATGATATA 1416
 QY 401 LysHisLeuGluLysGlyGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
 |||||
 Db 1417 AACCATTTGAGACGATGTGAACATCGATCATGGAATCCCTTGACATGGCTCTCAGATTCA 1476
 QY 421 ProLeuPheAspLeuIleLysGluSerLysAspArgGluGlyProThrAspHisLeuGlu 440
 |||||
 Db 1477 CCTTTATTGATCTTATTAACATCAAGACCGAGAGACAGACAGACATGATCCTTGAA 1536
 QY 441 SerAlaCysPProLeuAsnLeuPProLeuGlnAsnAsnHisThrAlaAlaAspMetCysLeu 460
 |||||
 Db 1537 TCTGCTTGCTCTTAATCTCTCTCCAGAAATTAATCAGACATGACAGCAATATGATCTT 1596
 QY 461 SerProValArgSerProLysLysLysGlySerThrArgValAsnSerThrAlaAsn 480
 |||||
 Db 1597 TCTCTGTGAAGATCTCCAAAGAAAAAGTTCAACTACGCGTGAATTTCTACTGCAAAAT 1656
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 |||||
 Db 1657 GCGAGACACACAGCAACCTCAGCTTCCAGACCCAGAGCCCATTAATCTACCTCTCTT 1716
 QY 501 SerLeuPheTyrLysLysValIleTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
 |||||
 Db 1717 TCACTGTTTTAAATAAAAGTATCGGCTAGCCCTATCTCGGCTAAATACACTTTGGAA 1776
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
 |||||
 Db 1777 CGCCTTCTGTGAGACACCCAGAAATAGAACATATCATCTGGACCCCTTTCAGACACCC 1836
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
 |||||
 Db 1837 CTCGAAATAGATAGAACTCATGAGAGACAGCATTTGGACCAATTATGATGTCTCC 1896
 QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValIleThrAla 580
 |||||
 Db 1897 ATGTATGCGCATATGCAAGATGAGAAATATAGACCTTAATCAAAATCATGTTGAACGCA 1956
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
 |||||
 Db 1957 TACAAAGATCTCTCATGCTGTTCAGAGAGACATCAACAGTGTGTTGATCAAGAAAGAG 2016
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 |||||
 Db 2017 GAGTATGATCTTATATAGTATTTCTATACCTCGGTCTTCATGCAAGACTGAAACAAAT 2076
 QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 |||||
 Db 2077 ATTTTCAAGATGCTTCACAGAGCCCTACCTTGTCACCAATACCTCAATTCCTCGA 2136
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
 |||||
 Db 2137 AGCCCTTAACAAGTTCTAGTTCAACCTTACGGATTCCTGAGAGGAACTCATATTTCGA 2196
 QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
 |||||
 Db 2197 CCCCTGAAGTCCATATTAATTTTCAGAGGCTGTCACACACACAAATAATGCTCTCA 2256
 QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
 |||||
 Db 2257 AGATTCAGAGATCTAGTATCAATTTGGTGAATCATTCGGGCACTTCAGAAAGTCCAGAAA 2316
 QY 701 IleAsnGlnMetValCysAsnSerAspArgValIleuLysArgSerAlaGluGlySerAsn 720
 |||||
 Db 2317 ATAAATCAAGATGTATGTACAGGACGACGATGTGCTCAAAAGAGTCTCAAGAGAAC 2376
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740

Db 2237 CCGCTTAACGACGTGAAAACTACGCTTTGATATGAAAGATCGAGATGACGAGATGCA 2436
 |||||
 QY 741 SerLysIleLeuProGlyLysSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 |||||
 Db 2437 AGTAAACATCTCCAGAGACTCCAAATTTTCAGCAGAACTGCGAGAAATGACTTCTACT 2496
 QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
 |||||
 Db 2497 CGAACACGAAATCAAAAGCAAGAAATGAAATGATGATGATGATGATGATGATGATG 2556
 QY 781 Lys 781
 |||||
 Db 2557 AAA 2559
 |||||
 RESULT 15
 AAV58446 standard; DNA; 3323 BP.
 ID AAV58446 standard; DNA; 3323 BP.
 AC AAV58446;
 AC AAV58446;
 DT 02-DEC-1998 (first entry)
 XX
 XX
 DE Modified retinoblastoma tumour suppressor gene.
 XX
 KM Modified retinoblastoma tumour suppressor; RPS protein; cancer therapy;
 KM cellular proliferation inhibitor; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 FT Key Location/Qualifiers
 FT CDS 7..2562
 FT /*tag= a
 XX
 FN MO9837091-A2.
 XX
 XX
 PD 27-AUG-1998.
 XX
 PF 19-FEB-1998; 98MO-US03041.
 XX
 PR 20-FEB-1997; 97US-0038118.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Benedict WF, Hu S, Xu H, Zhou Y;
 XX
 DR WPI: 1998-480788/41.
 DR P-PSDB; AAM69370.
 XX
 FT Retinoblastoma suppressor protein with N-terminal modification -
 FT Inhibiting cellular proliferation, particularly cancer
 XX
 PS Claim 22: Page 180-184; 249pp; English.
 XX
 CC This sequence encodes a modified retinoblastoma tumour suppressor
 CC protein (RPS) of the invention. The proteins can be used for inhibiting
 CC cellular proliferation, when coadministered with a p53 protein. The RPS
 CC can be used for treating diseases characterised by abnormal cellular
 CC proliferation, particularly cancers. The RPSs have a broader spectrum of
 CC activity than wild type RPSs.
 XX
 SO Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T; 0 other;
 SO
 Alignment Scores:
 Pred. No.: 0
 Score: 4017.00
 Length: 3323
 Matches: 781
 Percent Similarity: 100.00%
 Conservative: 0
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 100.00%
 Indels: 0
 Gaps: 0
 DB: 19
 US-09-026-459a-37 (1-781) x AAV58446 (1-3323)

Qy	1	MeSerAsgLysLeuLeuLysLysTyrAspValIleuPheAlaLeuPheSerLysLeuLuglyr	20
Db	217	ATGTCAACAGCTGTGMAAGAAAGTATGATGATTTGCTTGACCTTCAGCAAAATTGGAAAG	276
Qy	21	ThrCysGluLeuLleIeTyrLeuThrInPProSerSerSerLleSerThrGluLeuSer	40
Db	277	ACATGTGAACCTTATATATTTGGACAACAACCAAGCTTGATCTGACATAATTAATCT	336
Qy	41	AlaLeuValLeuLysValSerTPrLleThrPheLeuLeuAlaLysGluValLeuGln	60
Db	337	GCATGTGCTCTAAAGTTCTTGAGACACATTTTATAGCTAAAGAGGACGATTAACA	396
Qy	61	MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheLe	80
Db	397	ATGGAAAGATCTGTGATTTCAATTTCAGTTAAAGCATGTCGTCTGACATATTTAT	456
Qy	81	LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn	100
Db	457	AAACTCTCACCTCCCATGGTGTCTCAAGAACCATATAAACAGCTGTATTACCCATAT	516
Qy	101	GlySerProArgThrProLysArgGlyGlnAsnAspSerAlaArgLleAlaLysGlnLeu	120
Db	517	GGTTCACCTCCGAACCCAGGACGGTCCAGAACAGATGACGACGATAGCAAAACATA	576
Qy	121	GluAsnAspThrArgLleIleGluValLeuCysLysGluGlnLysGlyAsnLleAspGlu	140
Db	577	GAATAAGATACAAAGATATTATGAAAGTCTCTGTAAAGAACATGATATATATAGTAG	636
Qy	141	ValLysAsnValTyrThrLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr	160
Db	637	GTTAAAAAGTTATTCTTCAAAAATTTTAACTTTATAGATATCTCTGGACCTGTAACA	696
Qy	161	SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluLleTyrLeuLys	180
Db	697	TCTTAATGGACTTCCAGAGCTGTGAAAAATCTTTTAAACATACGAAAGAAATTAATCTTAA	756
Qy	181	AsnLysAspLeuAspAlaArgLeuPheLeuAspRhlAspLysThrLeuGlnThrAspSer	200
Db	757	ATTAAAGATCTAGAGCAAGATTTATTTTGGATCATGATTAACCTTCCAGACTGATCT	816
Qy	201	IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn	220
Db	817	ATGACACAGTTTGAACACCAACACACACACACCAAAATTAACCTTATGCAAGAGTGAT	876
Qy	221	ValIleProProIleThrProValArgThrValMetAsnThrIleGlnGlnLeuMetC	240
Db	877	GTAATTCCTCCACACACCTCCAGCTTAGAGCTGTATGAACAACATACCAACATTAATGATG	936
Qy	241	IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuLleSerTyrPheAsnAsnLys	260
Db	937	ATTTAAATTCGCAAGATGACAACTGCAGAAATCTGATTTCTATTTTAAACAATGC	996
Qy	261	ThrValAsnProLysGluSerLleLeuLysArgValLysAspLleGlyTyrIlePheLys	280
Db	997	ACAGTAATCCAAAAGAAAGATATCTGAAAAGAGGAAAGATATAGGATACATCTTTAA	1056
Qy	281	GlnLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys	300
Db	1057	GAGAAATTTTGTCTTAAGCTGTGGGACAGGGGTGTGTGCGAAATTTGATACAGCCATACAA	1116
Qy	301	LeuGluValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg	320
Db	1117	CTTGGAGTTCCGTTGATATTCGCGATTAAGGAATCCATGCTTAATCAGAAAGAACGA	1176
Qy	321	LeuSerLleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheIleMetSerLeuLeu	340
Db	1177	TTTATCAATTCAAAATTTTAGCAAACTTGTGATGACAAACATTTTTCATATGCTTTATG	1236
Qy	341	AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp	360
Db	1237	GCCTGGCGCTTGAGAGTGTATGTGCCACATATATACAGAAATACATCTCAGATCTTGAT	1296

QY	361	SGCGLYTHASPLESSEPHROTPPILELEASNVILLEASNVLEUYSALAPHEAS	380
DB	1297	TCGGAGACAGATTTCTCTTCCAGGGATTCGTATGCTTAATTTAAAGCCTTGAT	1356
QY	381	PHETRYLSVALLEGJUSERPHEILEYSGALLUGJLYASNVLEUTHARGJLWETLIE	400
DB	1357	TTTTTAAAGAGTATGAAAGTTTTTTCACAAAGCAAGGCAACTTGCAAGAAAGATA	1416
QY	401	LYSHILEJGLIARCSGJLHLSARGLILEMETJUSERLEUALATPLEUSASPSER	420
DB	1417	AACATTTAGAACGATGGAACATCGAATCATGGAATCCCTGCATGCTCTCATATCA	1476
QY	421	PROLEUPHASPLOULEILYSGJLSINSELYASAPARGJUGJLYPROTHRAPHLSIEUGJL	440
DB	1477	CCCTTATTTGATCTTATTTAAACATCAAGAGACCGAGAGGACACTGTATCCCTTGAA	1536
QY	441	SERALECYSPROLEUASNVLEUPROLEUGJLNASNVHLSITHALALALASPMETRYLEU	460
DB	1537	TCGCTGTGCTCTTAATCTTCCTTCACAAATATCCACATCGACAGCATGATATGATCT	1596
QY	461	SERPROVALARGSERPROLYSLEYSGJLSERTHTRARGVALANSERTHRLAAN	480
DB	1597	TCCTCGTAAAGTCTCCAAANAAAAAGSTTCACTAGCGGTAAATTCCTGTGCAAT	1655
QY	481	ALAGJUTHGINALATHSERALAPHEGLNTHGINLYSPROLEUYSSETHSERLEU	500
DB	1657	GCGAGACACAAAGCAACCTCAGCCTTCACACCCCAAGCACTTGTAAATCTACTCTCT	1716
QY	501	SERLEUPHETRYLSLEYVALTYTRARGJLEUALATYTRLEUARGJLEUANTRHLEUCYSGJL	520
DB	1717	TCACGTGTTTTTAAATAAAAGTGATATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTAA	1776
QY	521	ARGJLEUENSEGJLHLSAPROGJLLEJGLHLSLILEETPRTHLEUPHAGJLHLSH	540
DB	1777	CGCCTTGCTGTGAGACACCAGAAATTTAGAACATATCATCTGACCCCTTTCCAGCACAC	1836
QY	541	LEUGJLANSGLUTHYSGJLLEMETFARGASPARHLSLEAUGJLILEMETBACYSSE	560
DB	1837	CTCGAGATATGATATGAACCTATAGAGACAGCACTTTGACCAATTTATGATGTCTCC	1896
QY	561	METRYLEJLIECYSLEYVALLYASNVILASPLEULYSPHEJLSLILEVALTHRALA	580
DB	1897	ATGATATGGCATATGCAAAAGTAMAAATATGACCTTAAATTCAAATCATTTGATACAGCA	1956
QY	581	TYTILYASPLEUPROHIALVALJGLJLTHPHELYSARGVALLEULIELYSGJLUGJL	600
DB	1957	TACAGGATCTTCCTCATGCTGCTTCAGAGACATCTCAACGCTTTGATCAAAAGAGAG	2016
QY	601	GLUTHYASPSERLILEVALPHETRYASNSERVAPHMEGJLNAJGJLEULYSTRAN	620
DB	2017	GAGATGATCTTATATATGATTTCTATATCTGCTTATATGACAGCATTAACAAAT	2077
QY	621	ILEJGLNTHYALASERTHARGPROPTHNLEUSERPROILEPROHLSILEPORAG	640
DB	2077	ATTTTTCAGATATGCTTCCACACGAGCCCCCTTACCTTCACCAATACCTCATCTCTGCA	2136
QY	641	SESPROTYTISAPHEPROCESERPROLEUARGJLEPROGJLYASNVILETRYLIESER	660
DB	2137	AGCCCTTACAGTTCTCTATGTTCAACCTTCAGGATTCCTGAGAGGSAACATCTAATTCA	2196
QY	661	PROLEUYSSEPROTYLISLIESERGLUGJLEUPROTHPROTHLYSMETTRPRO	680
DB	2197	CCCCGAGAGGTCCATATPAAAATTTCCAGAGGTCTCCAAACCAACAAAATATGACTCCA	2255
QY	681	ARGSERATJLEULEVALSERILEJGLJUSERPHEJLTHSERGLUTYSPHEGJLNY	700
DB	2257	AGATCAAGAACTTATGATCAATTCATTTGCGATTCATCTCGGCACTTCGAGAGTTCCAGAAA	2316
QY	701	ILEASGLIMETVALCYASNSERSASPARVALLEULYASERSERJLAGJUGJYSERAN	720
DB	2317	ATTAATTCAGATGTATATGATACAGCACCGCTGCTCAAAAAGAGCTCGAAGAGAACACAC	2377
QY	721	PROBOLYSPROLEUYSLEYUALARGPHEASPILEGJLYSERASPGJLUALASPGJL	740

Db 2377 CCTCTAAACCACTGAAAACTACGCTTGATATGTAAGATCAGATGAAGCAGATGA 2436
QY 741 SerLysHisLeuProGlySerLysPheGlnLysLeuAlaGluMetThrSerThr 760
Db 2437 AGTAACATCTCCCGAGAGAGTCCAAATTTCACGAGAACTGGCAAAATGACTTCTACT 2496
QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
Db 2497 CGAACACGAAATGCAAAAGCAGAAAATGATGATAGCATGATACCTCAACACAGGAAAGAG 2556
QY 781 Lys 781
Db 2557 AAA 2559

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